

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 22:22:25 ; Search time 2799.87 Seconds
(without alignments)
3778.556 Million cell updates/sec

Title: US-09-196-427-2

Perfect score: 489

Sequence: 1 ATGAGATTTCGAACACCA.....TGTTCAACACACTTCTTGA 489

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	489	100.0	489	1	PCT-US01-04130A-2 Sequence 2, Appli
2	489	100.0	489	6	US-08-233-606-4 Sequence 4, Appli
3	489	100.0	489	9	US-08-504-042A-1 Sequence 1, Appli
4	489	100.0	489	9	US-08-567-342-1 Sequence 1, Appli
5	489	100.0	489	15	US-09-134-134-2 Sequence 2, Appli
6	489	100.0	489	29	US-09-724-841-1 Sequence 1, Appli
7	489	100.0	489	29	US-09-724-848-2 Sequence 2, Appli
8	489	100.0	489	29	US-09-743-416-4 Sequence 4, Appli
9	489	100.0	1202	17	US-09-349-216-9 Sequence 9, Appli
10	489	100.0	1202	18	US-09-442-384A-569 Sequence 2909, Ap
11	489	100.0	1202	21	US-09-543-679A-2909 Sequence 1, Appli
12	489	100.0	1202	32	US-09-849-014-1 Sequence 1, Appli
13	489	100.0	1346	60	US-60-213-360-743 Sequence 1761, Ap
14	489	100.0	1615	56	US-60-172-373-1761 Sequence 4211, Ap
15	489	100.0	1630	71	US-60-324-185-4211 Sequence 2912, Ap
16	489	100.0	17904	21	US-09-543-679A-2912 Sequence 65, Appl
17	487.8	99.8	1126	29	US-09-758-457-65 Sequence 5, Appli
18	487.4	99.7	489	18	US-09-437-585-5 Sequence 7, Appli
19	481	98.4	489	18	US-09-437-585-7 Sequence 1, Appli
20	465	95.1	489	6	US-08-233-606-1 Sequence 1, Appli
21	465	95.1	489	15	US-09-134-134-1 Sequence 4, Appli
22	465	95.1	489	29	US-09-724-841-4 Sequence 1, Appli
23	465	95.1	489	29	US-09-724-848-1 Sequence 3, Appli
24	465	95.1	489	29	US-09-743-416-3 Sequence 1486, Ap
25	451.4	92.3	453	14	US-09-016-434-1486 Sequence 28, Appl
26	405.4	82.9	694	29	US-09-758-457-28 Sequence 44336, A
27	400	81.8	409	17	US-09-362-510-44336 Sequence 44336, A
28	400	81.8	409	17	US-09-362-510A-44336 Sequence 44336, A
29	400	81.8	409	34	US-09-904-013-44336 Sequence 965, App
30	380	77.7	643	14	US-09-023-655-965 Sequence 15309, A
31	380	77.7	2165	56	US-60-172-373-15309 Sequence 15309, A

32 378.4 77.4 1248 1 PCT-US99-19607-1 Sequence 1, Appli
 33 378.4 77.4 1248 2 US-09-543-679A-2908 Sequence 2908, Ap
 34 378.4 77.4 1248 32 US-09-856-748-1 Sequence 1, Appli
 35 358 73.2 358 16 US-09-221-481-572 Sequence 572, App
 36 358 73.2 358 18 US-09-442-384-154 Sequence 154, App
 37 358 73.2 358 18 US-09-442-385-861 Sequence 861, App
 38 357 73.0 357 18 US-09-442-384-154 Sequence 154, App
 39 351.6 71.9 486 21 US-09-543-679A-2911 Sequence 2911, Ap
 40 345 70.6 345 29 US-09-724-841-12 Sequence 12, Appl
 41 337 68.9 1244 75 US-06-360-207-16948 Sequence 16948, A
 42 325.8 66.6 345 29 US-09-724-841-13 Sequence 13, Appl
 43 141.6 29.0 14968 1 PCT-US01-04130A-1 Sequence 1, Appli
 44 141.6 29.0 14968 1 PCT-US01-04130A-1 Sequence 111, App
 45 141.6 29.0 14968 21 US-09-543-679A-2910 Sequence 2910, Ap

ALIGNMENTS

RESULT 1
 PCT-US01-04130A-2
 ; Sequence 2, Application PC/TUS0104130A
 ; GENERAL INFORMATION:
 ; APPLICANT: Genaisance Pharmaceuticals, Inc.
 ; APPLICANT: Nandabalan, Krishnan
 ; APPLICANT: Stephens, J. Claiborne
 ; APPLICANT: Chew, Anne
 ; APPLICANT: Anastasio, Allison
 ; APPLICANT: Denton, R. Rex
 ; TITLE OF INVENTION: POLYMORPHISMS IN THE INTERLEUKIN 15 GENE
 ; FILE REFERENCE: MMH-0048 PCT IL15
 ; CURRENT APPLICATION NUMBER: PCT/US01/04130A
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 60/181,059
 ; PRIOR FILING DATE: 2000-02-08
 ; NUMBER OF SEQ ID NOS: 111
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 489
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 PCT-US01-04130A-2

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 Best Local Similarity 100.0%; Pred. No. 7.7e-110;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTACTT 60
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QY 241 CCCAGTTCGAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTATTATTCATT 300
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QY 301 GAGTCCCGAGATGCAAGTATTCATGATACAGTAGAAAAATCTCATCATCTAGCAAAACAC 360
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QY 481 ACTCTTTGA 489
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RESULT 2
 US-08-233-606-4
 ; Sequence 4, Application US/08233606
 ; GENERAL INFORMATION:
 ; APPLICANT: Grabstein, Kenneth
 ; APPLICANT: Anderson, Dirk
 ; APPLICANT: Eisenman, June
 ; APPLICANT: Fung, Victor
 ; APPLICANT: Rauch, Charles
 ; TITLE OF INVENTION: Epithelium-derived T-cell Factor
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/233,606
 ; FILING DATE: 22-APR-1994
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/031,399
 ; FILING DATE: 08-MAR-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Launer, Charlene
 ; REGISTRATION NUMBER: 33,035
 ; REFERENCE/DOCKET NUMBER: 2811
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 206-587-0430
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 489 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..489
 US-08-233-606-4

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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
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; LOCATION: 1..489
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US-09-134-134-2
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; APPLICATION NUMBER: US/09/134,134
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/392,317
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-134-2

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Best Local Similarity 100.0%; Pred. No. 7.7e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 6
US-09-724-841-1
; Sequence 1, Application US/09724841
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
```

Anderson, Dirk
Eisenman, June
Fun, Victor
Rach, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,841

FILING DATE: 29-Nov-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/189,193

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/393,305

FILING DATE: 22-FEB-1995

ATTORNEY/AGENT INFORMATION:

NAME: Mcmasters, David D.

REGISTRATION NUMBER: 33,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-622-4900

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..489

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-724-841-1

Query Match 100.0%; Score 489; DB 29; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.7e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTCGAAACACCATTTGAGAGATTTCCATCCAGTGTCTACTTGTGTTTACTT 60

DB 1 ATGAGATTCGAAACACCATTTGAGAGATTTCCATCCAGTGTCTACTTGTGTTTACTT 60

QY 61 CTAACAGTCATTTCTAACTGAAGTGGCATTGCTTCTCATTTTGGGCTGTTTCACT 120

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DB 361 AGTTTGTCTTCTAATCGGGAATGTACAGAAATCTGGATGCAAGAAATCTGAGGAATGGAG 420
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DB 481 ACTTCTTGA 489

RESULT 7

US-09-724-848-2

Sequence 2, Application US/09724848

GENERAL INFORMATION:

APPLICANT: Grabstein, Kenneth

Paxton, Raymond

Pettit, Dean

TITLE OF INVENTION: Antagonists of IL-15

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: Word for Windows 95, 7.0

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,848

FILING DATE: 28-Nov-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/134,134

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Malaska, Stephen L.

REGISTRATION NUMBER: 32,655

REFERENCE/DOCKET NUMBER: 2831

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0430

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 1..489

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-09-724-848-2

Query Match 100.0%; Score 489; DB 29; Length 489;
Best Local Similarity 100.0%; Pred. No. 7.7e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTCGAAACACCATTTGAGAGATTTTCCATCCAGTGTCTACTTGTGTTTACTT 60

DB 1 ATGAGATTCGAAACACCATTTGAGAGATTTTCCATCCAGTGTCTACTTGTGTTTACTT 60

QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTTCTTCAATTTTGGGCTGTTTCACT 120

DB 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTTCTTCAATTTTGGGCTGTTTCACT 120

Db 737 gaaaaataataaagaatttttgcagagttttgtacatatattgtccaaatgttcatcaac 796

QY 481 ACTCTTGA 489

Db 797 actcttga 805

RESULT 10

US-09-442-384A-569
; Sequence 569, Application US/09442384A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashov, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384A
; CURRENT FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384A-569

Query Match 100.0%; Score 489; DB 18; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTTACTTGTCTTACTT 60

Db 317 atgagatttcgaaacacatttgagaagtatttccatccagtgctacttgtttactt 376

QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTCATGCTTCTTCTTGGCTGTTTCAGT 120

Db 377 ctaaacagtcattttctaaactgaagtggcattcatgtcttcttgggctgttccagt 436

QY 121 GCAGGGCTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATT 180

Db 437 gcagggttcttaaacagagccaaactgggtgaatgtaataagtatttgaaaaaatt 496

QY 181 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 240

Db 497 gaagatcttattcaatctatgcatattgactgacttataatatacggaaagtgttccac 556

QY 241 CCCAGTGGCAAGTAAACAGCAATGAAGTGGCTTCTTCTTGGAGTTACAGTTATTTTCACTT 300

Db 557 cccagtgcaagtaaacagcaatgaagtggcttcttcttggagttacaagtatttccactt 616

QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATAATCTGATCATCTAGCAACAAC 360

Db 617 gagtccggagatgcaagtattcatgatacagtagaataatctgatactctagcaacaac 676

QY 361 AGTTTCTTCTTAATCGGAATGPAACAGATCTGATGATGATGATGATGATGATGATGATG 420

Db 677 agtttcttctaattggaatgtaacagaatctggtgcaagaatgtgaggaaactggag 736

QY 421 GAAAAAATATTAAGAAATTTTGGAGAGTTTGTGATACATATTTCCAAATGTTTCATCAAC 480

Db 737 gaaaaataataaagaatttttgcagagttttgtacatatattgtccaaatgttcatcaac 796

QY 481 ACTCTTGA 489

Db 797 actcttga 805

RESULT 11

US-09-543-679A-2909
; Sequence 2909, Application US/09543679A
; GENERAL INFORMATION:

APPLICANT: NYCE, Jonathan W.
TITLE OF INVENTION: LOW ADENOSINE ANTI-SENSE OLIGONUCLEOTIDE,
COMPOSITIONS, KIT & METHOD FOR TREATMENT
OF AIRWAY DISORDERS ASSOCIATED WITH
BRONCHOCOUSTRICTION, LUNG INFLAMMATION,
NUMBER OF SEQUENCES: 3111
CORRESPONDENCE ADDRESS:
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
STREET: 7 Clarke Drive
CITY: Cranbury
STATE: NJ
COUNTRY: USA
ZIP: 08512
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-R
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: N/A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/543,679A
FILING DATE: 13-Apr-2000
CLASSIFICATION: UNKNOWN
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/127,958
FILING DATE: 1998-08-03
ATTORNEY/AGENT INFORMATION:
NAME: Amzel, Viviana
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: EPI-0067191b
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-409-3035
TELEFAX: 413-254-9245
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2909:
SEQUENCE CHARACTERISTICS:
LENGTH: 1202 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2909:
US-09-543-679A-2909

Query Match 100.0%; Score 489; DB 21; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGATTTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTTACTTGTCTTACTT 60

Db 317 ATGAGATTTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTTACTTGTCTTACTT 376

QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTCATGCTTCTTCTTGGCTGTTTCAGT 120

Db 377 CTAACAGTCATTTTCTAACTGAAGTGGCATTCATGCTTCTTCTTGGCTGTTTCAGT 436

QY 121 GCAGGGCTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATT 180

Db 437 GCAGGGCTTCTAAAACAGAGCCAACTGGTGAATGTAATAGTATTTGAAAAAATT 496

QY 181 GAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 240

Db 497 GAAGATCTTATTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATG 556

QY 241 CCAGTGGCAAGTAAACAGCAATGAAGTGGCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 300

Db 557 CCAGTGGCAAGTAAACAGCAATGAAGTGGCTTCTTCTTGGAGTTACAAGTTATTTTCACTT 616

QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATAATCTGATCATCTAGCAACAAC 360

Db 617 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAATAATCTGATCATCTAGCAACAAC 676

QY 361 AGTTTCTTCTTAATCGGAATGTAACAGATCTGATGATGATGATGATGATGATGATGATG 420

Db 677 AGTTGTTCTTAATGGGATTAACAGAACTGGATGCAAGAAATGTGAGGAAGTGGAG 736
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 737 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 796
QY 481 ACTTCTTGA 489
Db 797 ACTTCTTGA 805

RESULT 12
US-09-849-014-1
; Sequence 1, Application US/09849014
; GENERAL INFORMATION:
; APPLICANT: BEN GURION UNIVERSITY OF THE NEGEV
; APPLICANT: MOR - RESEARCH APPLICATIONS LTD.
; TITLE OF INVENTION: ANTISENSE OLIGOMER
; FILE REFERENCE: A34255 PCT USA-A
; CURRENT APPLICATION NUMBER: US/09/849,014
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: IL126919
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-849-014-1

Query Match 100.0%; Score 489; DB 32; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-110;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAAATTCGAACCCACATTTGAGAGATATTTCCATCCAGTCTACTTGTGTTACTT 60
Db 317 atgagaatttcgaaccacatttgagaagatttccatccagtgctacttggtttactt 376
QY 61 CTAACAGCTCAATTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGTGTTTCAGT 120
Db 377 ctaaacagctcaatttctaactgaagctggcattcatgcttctcattttgggctgtttcagt 436
QY 121 GCAGGGCTTCTAAACAGAGCCCAACTGGGTGAATGTAATGATGATTTGAAAAAAT 180
Db 437 gcagggcttctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaaatt 496
QY 181 GAAGATCTTATTAATCTATCATATTCATGCTACTTATATACGGAAGTGAATGTTTCA 240
Db 497 gaagatcttatcaatctcatgcatatgtatgctactttatatacggaaagtgtgttca 556
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAGTTATTTCAC 300
Db 557 cccagttgcaagtaacagcaatgaagtgctttctcttggagttacaagttatttcaactt 616
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAAAGTCTGATCATCTCTAGCAAAAC 360
Db 617 gagtcggagatgcaagtatttcattgatcacagtagaataatctgatcctctcagcaaac 676
QY 361 AGTTTGCTTCTTAATGGAAATGTAACGAATCTGGATGCAAGAAATGTGAGGAAGTGG 420
Db 677 agtttgcttcttaattggaaatgtaacgaatctggatgcaagaagtgtgaggaactggag 736
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 737 gaaaaaatattaaagaatttttcagagttttgtacatattgtccaaatgttccatcaac 796
QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

RESULT 14
US-60-172-373-1761
; Sequence 1761, Application US/60172373
; GENERAL INFORMATION:

RESULT 13
US-60-213-360-743
; Sequence 743, Application US/60213360
; GENERAL INFORMATION:
; APPLICANT: MORRIS, MacDonald
; APPLICANT: Lai, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Poly
; TITLE OF INVENTION: Identified Thereby
; FILE REFERENCE: CX-0014 P
; CURRENT APPLICATION NUMBER: US/60/213,360
; CURRENT FILING DATE: 2000-06-21
; NUMBER OF SEQ ID NOS: 8347
; SOFTWARE: PERL Program
; SEQ ID NO 743
; LENGTH: 1346
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1082250.1
; NAME/KEY: unsure
; LOCATION: 1248
; OTHER INFORMATION: a, t, c, g, or other
US-60-213-360-743

Query Match 100.0%; Score 489; DB 60; Length 1346;
Best Local Similarity 100.0%; Pred. No. 1e-109;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAAATTCGAACCCACATTTGAGAGATATTTCCATCCAGTCTACTTGTGTTACTT 60
Db 136 atgagaatttcgaaccacatttgagaagatttccatccagtgctacttggtttactt 195
QY 61 CTAACAGCTCAATTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGTGTTTCAGT 120
Db 196 ctaaacagctcaatttctaactgaagctggcattcatgcttctcattttgggctgtttcagt 255
QY 121 GCAGGGCTTCTAAACAGAGCCCAACTGGGTGAATGTAATGATGATTTGAAAAAAT 180
Db 256 gcagggcttctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaaatt 315
QY 181 GAAGATCTTATTAATCTATCATATTCATGCTACTTATATACGGAAGTGAATGTTTCA 240
Db 316 gaagatcttatcaatctcatgcatatgtatgctactttatatacggaaagtgtgttca 375
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTTGGAGTTACAAGTTATTTCAC 300
Db 376 cccagttgcaagtaacagcaatgaagtgctttctcttggagttacaagttatttcaactt 435
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAAAGTCTGATCATCTCTAGCAAAAC 360
Db 436 gagtcggagatgcaagtatttcattgatcacagtagaataatctgatcctctcagcaaac 495
QY 361 AGTTTGCTTCTTAATGGAAATGTAACGAATCTGGATGCAAGAAATGTGAGGAAGTGG 420
Db 496 agtttgcttcttaattggaaatgtaacgaatctggatgcaagaagtgtgaggaactggag 555
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 556 gaaaaaatattaaagaatttttcagagttttgtacatattgtccaaatgttccatcaac 615
QY 481 ACTTCTTGA 489
Db 616 acttcttga 624


```

; APPLICANT: Morris, MacDonald
; APPLICANT: Lai, Preeti
; APPLICANT: Disp, Dinh
; TITLE OF INVENTION: Method for the Identification of Sequence Polymorphisms Using
; TITLE OF INVENTION: Polynucleotide Sequence Databases, and Single Nucleotide Polymorp
; FILE REFERENCE: GX-0006 P
; CURRENT APPLICATION NUMBER: US/60/172,373
; CURRENT FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 25,772
; SOFTWARE: PERL Program
; SEQ ID NO 1761
; LENGTH: 1615
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 348901.2
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 104, 1517
; OTHER INFORMATION: a, t, c, g, or other
US-60-172-373-1761

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Query Match	100.0%;	Score 489;	DB 56;	Length 1615;
Best Local Similarity	100.0%;	Pred. NO. 1.1e-109;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGAATTTCGAACACACATTTGAGAAAGTATTTCATCCAGTCTACTTGTGTTTACTT	60	
DB	405	atgagaatttcgaacacacatttgagaagtatttccatccagtgctacttggttcaact	464	
QY	61	CTAAACAGTCAATTTCTAAACTGAAGCTGGCATTCATGCTTCTCATTTTGGGCTGTTTCAGT	120	
DB	465	ctaaacagtcattttcttaactgaagctggcattcatgtcttcattttgggctgtttcaagt	524	
QY	121	GCAGGGTTCTCTAAACAGAAAGCCAACTGGGTGAATGTAAATAGTAAATTCGAAAAAATT	180	
DB	525	gcagggttctctaaacagaaagccaactgggtgaatgtaataagtgattgaaaaaaatt	584	
QY	181	GAAGATCTTATTCAATCTATGCATATTGACTACTTATATACGGAAAGTANGTTTCAC	240	
DB	585	gaagattttatccaattcattgcattgactgactttatatacggaaagtgagtctcac	644	
QY	241	CCCAGTTGCAAAAGTAACAGCAATGAAGTGCCTTCTCTGGAGTACAAAGTATTTCACCT	300	
DB	645	cccaagtgcgaagTaaacagcaatgaagtgccttctcttggagttacaagttatttcactt	704	
QY	301	GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCCTTAGCAAAACAC	360	
DB	705	gagtcggagatgcaagtattcatgacagttagaaaactgatcatcctagcaaacac	764	
QY	361	AGTTTGTCTCTAATGGGAATGTAAACAAATCTCGATGCAAGAAATGTGAGGAAGTGGAG	420	
DB	765	agttctgtctcttaattgggaatgaacagaaacctggatgcaagaagtgcaggaactggag	824	
QY	421	GAATAAATATTAAGAAATTTTTCAGAGTTTTGTACATATGTGCCAAATGTTCATCAAC	480	
DB	825	gaaaaaatattaagaatttttgcagagttttgtacatatgtgccaaatgttcatcaac	884	
QY	481	ACTTCTTGA	489	
DB	885	acttcttga	893	

RESULT 15
US-60-324-185-42H1
; Sequence 4211, Application US/60324185
; GENERAL INFORMATION:
; APPLICANT: Morris, MacDonald
; APPLICANT: Lal, Preeti
; APPLICANT: Diep, Dinh
; TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF SEQUENCE POLYMORPHISMS USING

```

; TITLE OF INVENTION: POLYNUCLEOTIDE SEQUENCE DATABASES, AND SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS IDENTIFIED THEREBY
; FILE REFERENCE: GX-0019-1 P
; CURRENT APPLICATION NUMBER: US/60/324,185
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 35862
; SOFTWARE: PERL Program
; SEQ ID NO 4211
; LENGTH: 1630
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1082250.1
; NAME/KEY: unsure
; LOCATION: 1532
; OTHER INFORMATION: a, t, c, g, or other
US-60-324-185-4211

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Query Match          100.0%; Score 489; DB 71; Length 1630;
Best Local Similarity 100.0%; Pred. No. 1.1e-109;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	1	ATGAGAAATTTGAAACACACATTTGAGAAGTATTTCATCCAGTGTACTGTGTTTACTT	60
DB	420	atgagaatttcgaaacacacatttgaagaagtatttccatccagtgctacttggttactt	479
QY	61	CTAAACAGTCAATTTCTAACTGAAGCTGGCATTCATGCTCTCATTTTGGCGCTGTTTCAGT	120
DB	480	ctaaacagtcattttcttaactgaagctggcattcatgtcttcatttggcgtgtttcagt	539
QY	121	GCAGGGCTTCCTAAACACAGAAGCCAACCTGGTGCAATGTAATAAGTCATTTGAAGAAATTT	180
DB	540	gcagggcttctctaaacacagaagccaactgggtgaatgtaataagtgatttgaagaaatt	599
QY	181	GAAGATCTTAATTCAAATCTATGTCATATTGATGCTACTTTATATACGGAAAGTGATGTTCACT	240
DB	600	gaagatcttattccaatctatgcatattgattgctacttataacggaagaagtgaattcaac	659
QY	241	CCAGTTGCAAAATTAACAGCAATGAAGTGGTCTTCTCTGGAGTTACAAATTTATTTCACTTT	300
DB	660	ccagttgcgaagttaacagcaatgaagtgcttctctcttggagttaacagttatttcaactt	719
QY	301	GAGTCCGGAGATCAAGTATTCAATGATACAGTAGAANAATCTGATCATCTCAGCAACACAC	360
DB	720	gagtcoggagatcgaagtatctatgatacagtagaanaatctgatcatcctagacaacac	779
QY	361	AGTTTGTCTTCTAATGGGAATGTAACAGCAATCTGGAATGCAAGAAATGTGAGGAACCTGGAG	420
DB	780	agtttgtctctaatgggaatgtaaacagaatctcgagatgcaagaagaatgtgagggaactggag	839
QY	421	GAAAAAATATTAAAGAAATTTTTCAGAGTTTTGTACATATTGTCCAAATGTTCAATCAAC	480
DB	840	gaaaaaaattaaagaatttttgcagagtttggatcatatgtgccaaatgttccatccaac	899
QY	481	ACTCTCTGA	489
DB	900	acttctctga	908

Search completed: September 20, 2002, 00:12:06
Job time: 6581 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 22:49:15 ; Search time 310.08 Seconds
(without alignments)
5039.363 Million cell updates/sec

Title: US-09-196-427-2
Perfect score: 489
Sequence: 1 ATGAGAAATTCGAAACACCA.....TCTTCATCAACACTTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2129675 seqs, 1597756363 residues

Total number of hits satisfying chosen parameters: 4259350

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	100.0	489	5	US-09-855-313A-3
2	489	100.0	489	5	US-09-953-323A-3
3	489	100.0	1202	5	US-09-053-375B-567
4	487.8	99.8	1126	6	US-09-442-384B-569
5	487.8	99.8	1126	6	US-10-219-925-65
6	482.6	98.7	489	5	US-09-855-313A-1
7	482.6	98.7	489	5	US-09-953-323A-1
8	405.4	82.9	694	6	US-10-219-925-28
9	358	73.2	358	5	US-09-442-366A-1102
10	357	73.0	357	5	US-09-442-384B-154
11	337	68.9	1250	5	US-09-053-375B-1144
12	332.2	67.9	1313	6	US-10-191-803-72
13	157.8	32.3	285	5	US-09-454-226A-527
14	116	23.7	181	6	US-10-216-086-422
15	102.6	21.0	565	7	US-10-106-698-2528
16	72.4	14.8	472	5	US-09-918-995-25100
17	60	12.3	60	5	US-09-908-975A-11280
18	45.6	9.3	60	5	US-09-855-313A-7
19	45.6	9.3	60	5	US-09-953-323A-7
20	40	8.2	1933	7	US-10-018-902-15
21	38.8	7.9	1024	7	US-10-027-632-253434
22	38.8	7.9	1024	7	US-10-027-632-253435
23	37.6	7.7	2547	7	US-10-179-131-116
24	36.8	7.5	1227	7	US-10-179-131-4956
25	36.8	7.5	2074	5	US-09-629-469A-11837

ALIGNMENTS

RESULT 1

US-09-855-313A-3
; Sequence 3, Application US/09855313A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Maslinski, Wlodzimierz
; APPLICANT: Zheng, Xin Xiao
; APPLICANT: Kim, Yon Su
; APPLICANT: Lacraz, Sylvie Ferrari
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ACHIEVING IMMUNE SUPPRESSION
; FILE REFERENCE: 01948-056001
; CURRENT APPLICATION NUMBER: US/09/855,313A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/203,801
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-855-313A-3

Query Match 100.0%; Score 489; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 8.3e+108; Mismatches 0; Indels 0; Gaps 0;
Matches 489; Conservative 0

QY 1 ATGAGAAATTCGAAACCAACATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTACTT 60
Db 1 atgagaatttcgaaccacacatttgagaagtatttccatccagtgctacttgtgttactt 60
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCAATTCATGCTCTTCATTTTGGGCTGTTTCAGT 120
Db 61 ctaacagtcatttcttaactgaagctggcattcattcttcttcttcttcttcttcttcttctt 120
QY 121 GCAGGGTCTCTAAACAGACCAACTGGTGAATGTAATGAAGTATTTCGAAAAAATTT 180
Db 121 gcagggtctcttaaacagacccaactggctgaatgtaatgaagtgatgaatgaatgaatgaat 180
QY 181 GAAGATCTTATTCATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 gaagatcttattcaatctatgctatgctatgctatgctatgctatgctatgctatgctatgctac 240
QY 241 CCCAGTGCAGAAAGTAACAGCAATGAAGTCTTCTCTCTGGAGGATTAAGTATTTCATTTTCACTT 300

```
|||||
Db 241 ccagttgcaagtaacagcaatgaagtgtcttctcttgaggtacaaagtatttcaactt 300
QY 301 GAGTCGGAGATCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 301 gagtcggagatgcaagtattcatgatagagaaatctgatcatctctagcaaacac 360
QY 361 AGTTTCTCTTAATCGGAGATGTAACAGAACTGGATGCAAAAGATGTGAGGAATGGAG 420
Db 361 agttgtctcttaattgggaatgtaacagaatctggatgcaagaaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTATTGTACATATGTCACAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaattttgagagcttttgcacattgttccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 2
US-09-953-323A-3
; Sequence 3, Application US/09953323A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Li, Xian Chang
; TITLE OF INVENTION: MODULATION OF IL-2 AND IL-15 MEDIATED T CELL RESPONSES
; FILE REFERENCE: 01948-057001
; CURRENT APPLICATION NUMBER: US/09/953,323A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/232,251
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-953-323A-3
```

```
Query Match 100.0%; Score 489; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 8.3e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGCAAAACCCACATTTGAGAAGTATTTCATCCAGTGTCTACTTGTGTTACTT 60
Db 1 atgagaatttcgaaacccaccatttggagaagtatttccatccagtgctacttggtttactt 60
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCAATCATGTCTTCAATTTGGGCTGTTTCAGT 120
Db 61 ctacacagtcattttctaactgaagctggcattcatcttcttcatcttgggctgtttcagt 120
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTATTGAAAAAAT 180
Db 121 gcagggtctctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaatt 180
QY 181 GAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTATGATCTTCAAC 240
Db 181 gaagatcttatttcattctatgctatgtacttttataacggaagtatgattttcact 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTTCAC 300
Db 241 cccagttgcaagtaaacagcaatgaagtgtcttctcttggagttacaagttatttcaactt 300
QY 301 GAGTCGGAGATGCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 301 gagtcggagatgcaagtatttcattgatcacagttagagaaatctgatcatctctagcaaacac 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAAATCTGGATCAAAAGATGTGAGGAATGGAG 420
```

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|||||
Db 361 agttgtctctctcaagggaatgaacagaatctggtgcaagaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTATTGTACATATTGTCCAAATGTTCAATCAAC 480
Db 421 gaaaaaataattaaagaattttgcagagtttgcacattgtgtacattgtccaaatgttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 3
US-09-053-375B-567
; Sequence 567, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 567
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-053-375B-567
```

```
Query Match 100.0%; Score 489; DB 5; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAATTTGCAAAACCCACATTTGAGAAGTATTTCATCCAGTGTCTACTTGTGTTACTT 60
Db 317 atgagaatttcgaaacccaccatttggagaagtatttccatccagtgctacttgtgttactt 376
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCAATCATGTCTTCAATTTGGGCTGTTTCAGT 120
Db 377 ctacacagtcattttctaactgaagctggcattcatcttcttcatcttgggctgtttcagt 436
QY 121 GCAGGGCTTCTAAACAGAGCCAACTGGGTGAATGTAATGAAGTATTGAAAAAAT 180
Db 437 gcagggtctctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaatt 496
QY 181 GAAGATCTTATTCATCTATGATGCTACTTTATATACGGAAGTATGATCTTCAAC 240
Db 497 gaagatcttatttcattctatgctatgtactttatatacgggaagtgtgttccac 556
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTATTTCAC 300
Db 557 cccagttgcaagtaaacagcaatgaagtgtcttctcttggagttacaagttatttcaactt 616
QY 301 GAGTCGGAGATGCAAGTATTCAATGATACAGTAGAGAAATCTGATCATCTTAGCAACAAC 360
Db 617 gagtcggagatgcaagtatttcattgatcacagttagaaaaatctgatcatctctagcaaacac 676
QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAAATCTGGATCAAAAGATGTGAGGAATGGAG 420
Db 677 agttgtctctctcaagggaatgtaacagaatcttggatgcaagaatgtgaggaactggag 736
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTATTGTACATATTGTCCAAATGTTCAATCAAC 480
Db 737 gaaaaaataattaaagaattttgcagagtttgcacattgttccaaatgttcatcaac 796
QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

RESULT 4
```

US-09-442-384B-569
; Sequence 569, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashiev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 569
; LENGTH: 1202
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-442-384B-569

Query Match 100.0%; Score 489; DB 5; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.9e-108;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTTTACTT 60
Db 317 atgagaaattcgaaacacacatttgagaagtatttccatccagtgctacttggtttactt 376
QY 61 CTAAACAGTCTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTCTTTTCAGT 120
Db 377 ctaaaacagtcattttctaactgaagctggcattcatgcttcttcaattttgggctggtttcagtt 436
QY 121 GCAGGGCTTCTTAAACAGAACCAACTGGGTGAATGTATAAAGTGAATTTGAAAAAAATTT 180
Db 437 gcagggtcttcttaaaacagaaagccaactgggtgaatgtaataagtgatttgaaaaaaatt 496
QY 181 GAGATCTTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGTATTCAC 240
Db 497 gaagatcttattcaatctatgatatgtatgctactttatatacggaaagtgtatgttcac 556
QY 241 CCCAGTTCGAAAGTAAACAGCAATGCTTCTTCTTGGAGTTACAAAGTTATTTTCACTT 300
Db 557 cccagttcgaaagtaaacagcaatgaagtcttctcttgagttacaagtatttcactt 616
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAGAAATCTGATCATCTAGCAAAACAAC 360
Db 617 gagtccggagatgcaagtattcatgatatgacagtagaagaaatctgatcatcctctagcaaaacaac 676
QY 361 AGTTTCTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
Db 677 agtttctcttaattgggaatgtaaacagaatctggatgcaagaaatgtgaggaactggag 736
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
Db 737 gaaaaaataatlaagaaatttttgcagagtttgtacatatgttgcataattgtccaaatgttcatcaac 796
QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

RESULT 5
US-10-219-925-65/c
; Sequence 65, Application US/10219925
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM042CJN
; CURRENT APPLICATION NUMBER: US/10/219,925
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 09/758,457
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065

; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 806
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 1126
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-925-65

Query Match 99.8%; Score 487.8; DB 6; Length 1126;
Best Local Similarity 99.4%; Pred. No. 1.9e-107;
Matches 486; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTTTACTT 60
Db 826 atgagaaattcgaaacacacatttgagaagtatttccatccagtgctacttggtttactt 767
QY 61 CTAAACAGTCTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
Db 766 ctwaacartcatTTTCTTAACCTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 707
QY 121 GCAGGGCTTCTTAAACAGAACCAACTGGGTGAATGTATAAAGTGAATTTGAAAAAAATTT 180
Db 706 gcagggtcttcttaaaacagaaagccaactgggtgaatgtaataagtgatttgaaaaaaatt 647
QY 181 GAGATCTTATCAATCTATGATATTTGATGCTACTTTATATACGGAAGTGTATTCAC 240
Db 646 gaagatcttattcaatctatgatatgtatgctactttatatacggaaagtgtatgttcac 587
QY 241 CCCAGTTCGAAAGTAAACAGCAATGCTTCTTCTTGGAGTTACAAAGTTATTTTCACTT 300
Db 586 cccagttcgaaagtaaacagcaatgaagtcttctcttgagttacaagtattttcactt 527
QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAGAAATCTGATCATCTAGCAAAACAAC 360
Db 526 gagtccggagatgcaagtatttcatgatatgacagtagaagaaatctgatcatcctctagcaaaacaac 467
QY 361 AGTTTCTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
Db 466 agtttctcttaattgggaatgtaaacagaatctggatgcaagaaatgtgaggaactggag 407
QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
Db 406 gaaaaaataatlaagaaatttttgcagagtttgtacatatgttgcataattgtccaaatgttcatcaac 347
QY 481 ACTTCTTGA 489
Db 346 acttcttga 338

RESULT 6
US-09-855-313A-1
; Sequence 1, Application US/09855313A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Maslinski, Wlodzimierz
; APPLICANT: Zheng, Xin Xiao
; APPLICANT: Kim, Yon Su
; APPLICANT: Lacraz, Sylvie Ferrari
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR ACHIEVING IMMUNE SUPPRESSION
; FILE REFERENCE: 01948-056001
; CURRENT APPLICATION NUMBER: US/09/855,313A
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/203,801
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 489
; TYPE: DNA

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-855-313A-1

Query Match

Best Local Similarity 98.7%; Score 482.6; DB 5; Length 489;
Matches 485; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTCCAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
Db 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttgtgtttactt 60
QY 61 CTAAACAGTCATTTCTTAAGTGAAGCTGGCATTTCTATGCTTTTGGGCTGTTTTCAGT 120
Db 61 ctaaacagtcattttcttaactgaagctggcattcattcttcttcttgggctgtttcagtt 120
QY 121 GCAGGGCTTCTTAAACAGAACCCCAACCTGGGTGAATGTAATGAAGTGTATTTGAAAAAATT 180
Db 121 gcagggtcttcttaaacagaaagcccaactgggtgaatgtaataagtgattgaaaaaaatt 180
QY 181 GAAGATCTTATTCAATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTCTTAC 240
Db 181 gaagatcttattcaatctatgctatttgcattcttatacaggaagtgattgttccac 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTGGAGTTTACAAGTTATTTCACTT 300
Db 241 ccagttgcaagtaaacagcaatgaagtgcttcttcttcttggagttacaagttatttcaatt 300
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGTATCATCTCTAGCAAAACAC 360
Db 301 gagtccggagatgcaagtatttcattcatgatacagtagaaaaatctgtatcctctagcaaaacac 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTACAGAACTGTGATGCAAGAAATGTGAGGAAGTGGAG 420
Db 361 agtttgtcttcttaatgggaatgtacagaactgtgatgcaagaaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 gaaaaaattattaaagaatttttgcagagtttgtacatattgtccaaatgtttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 7

US-09-953-323A-1
; Sequence 1, Application US/09953323A
; GENERAL INFORMATION:
; APPLICANT: Strom, Terry B.
; APPLICANT: Li, Xian Chang
; TITLE OF INVENTION: MODULATION OF IL-2 AND IL-15 MEDIATED T CELL RESPONSES
; FILE REFERENCE: 01948-057001
; CURRENT APPLICATION NUMBER: US/09/953,323A
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US 60/232,251
; PRIOR FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(486)
US-09-953-323A-1

Query Match

98.7%; Score 482.6; DB 5; Length 489;

Best Local Similarity 99.2%; Pred. No. 2.8e-106;
Matches 485; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGAGAAATTTCCAAACCCACATTTGAGAAGTATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
Db 1 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttgtgtttactt 60
QY 61 CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTTCTATGCTTTTGGGCTGTTTTCAGT 120
Db 61 ctaaacagtcattttcttaactgaagctggcattcattcttcttcttgggctgtttcagtt 120
QY 121 GCAGGGCTTCTTAAACAGAACCCCAACCTGGGTGAATGTAATGAAGTGTATTTGAAAAAATT 180
Db 121 gcagggtcttcttaaacagaaagcccaactgggtgaatgtaataagtgattgaaaaaaatt 180
QY 181 GAAGATCTTATTCAATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTCTTAC 240
Db 181 gaagatcttattcaatctatgctatttgcattcttatacaggaagtgattgttccac 240
QY 241 CCCAGTTGCAAGTAAACAGCAATGAAGTGTCTTCTTGGAGTTTACAAGTTATTTCACTT 300
Db 241 ccagttgcaagtaaacagcaatgaagtgcttcttcttcttggagttacaagttatttcaatt 300
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAATCTGTATCATCTCTAGCAAAACAC 360
Db 301 gagtccggagatgcaagtatttcattcatgatacagtagaaaaatctgtatcctctagcaaaacac 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTACAGAACTGTGATGCAAGAAATGTGAGGAAGTGGAG 420
Db 361 agtttgtcttcttaatgggaatgtacagaactgtgatgcaagaaatgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 gaaaaaattattaaagaatttttgcagagtttgtacatattgtccaaatgtttcatcaac 480
QY 481 ACTTCTTGA 489
Db 481 acttcttga 489

RESULT 8

US-10-219-925-28
; Sequence 28, Application US/10219925
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PM042C1N
; CURRENT APPLICATION NUMBER: US/10/219,925
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 09/758,457
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 806
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 694
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (651)
; OTHER INFORMATION: n equals a,t,g, or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (681)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-219-925-28

Query Match

82.9%; Score 405.4; DB 6; Length 694;

Best Local Similarity 97.4%; Pred. No. 9.9e-88; Mismatches 8; Indels 4; Gaps 3;
Matches 443; Conservative 0;

QY 1 ATGAGAAATTTCCAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTTTACTT 60
|||||
Db 241 atgagaatttcgaaccacacatttgagaagtatttccatccagtgctacttggttactt 300
QY 61 CTAAACAGTCATTTCTTAAGTGCATTCATGCTTCTTCTTGGAGTTACAAGTTATTTCACT 120
|||||
Db 301 ctaaacagtcattttcttaactgaagctggcattcattgtcttcttatttgggctgttcagt 360
QY 121 CGAGGCTTCCCTAAACAGACCACTGGTCAATGTAATAGTCAATTTGAAAAAAT 180
|||||
Db 361 gcagggtcttccctaaacagagcccaactggggaatgtaataagtatttgaaaaaatt 420
QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTATCTATATACGGAAGTGTATTCAC 240
|||||
Db 421 gaagatcttattcaactatgatcatattgatgctactttatatacaggaagtgttcac 480
QY 241 CCCAGTTGCAAGTACACAGATGAAGTCTTCTTCTTGGAGTTACAAGTTATTTCACTT 300
|||||
Db 481 cccagttgcaagtaacagcaatgaagtgtcttcttcttgaggtacaagttatttcaatt 540
QY 301 GAGTCCGGAGATCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAACAAC 360
|||||
Db 541 gagt-cggagatgcaagttatcatgatacagtagaatactctgatcatccttagcaaac 599
QY 361 AGTTCTCTTCTTAATGGAGTAAACAGAACTCT-GGATGCAAGAAATGTCAGGAAGTGG- 418
|||||
Db 600 agttgtcttcttaagtgaatgaacagaatctggatgccaaagaatglangaactggg 659
QY 419 -AGGAAAAAATATTAAAGAAATTTTTCAGAGTTT 452
|||||
Db 660 aggaataataatttaagaanttttgcagagttt 694

RESULT 9
US-09-442-366A-1102
; Sequence 1102, Application US/09442366A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey E.
; TITLE OF INVENTION: Human Array
; FILE REFERENCE: CLON-006CIP13
; CURRENT APPLICATION NUMBER: US/09/442,366A
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; NUMBER OF SEQ ID NOS: 2216
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1102
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene fragment
US-09-442-366A-1102

Query Match 73.2%; Score 358; DB 5; Length 358;
Best Local Similarity 100.0%; Pred. No. 2e-76;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTTCTTAAACAGTCAATTTCTTAAC 81
|||||
Db 1 ttgagaagtatttccatccagtgctacttggtttacttctaaacagtcattttcttaact 60
QY 82 GAAGCTGGCATTCATCTCTTCTTCTTCTTGGGCTGTTTTCAGTGCAGGGCTTCTTAAACAGAA 141
|||||
Db 61 gaagctggcatttcattctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 120
QY 142 GCCAACTGGGTGAATTAATAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATG 201
|||||
Db 121 gccaaactgggtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 180
QY 202 CATATTGATGCTACTTTATATAGCGGAAGTGTATTCACCCCAAGTGTGCAAGGTAACAGCA 261
|||||
Db 181 catattgatgctactttatatacggaaagtgtgttcaccccgagtggttcaccccgagtggttc 240
QY 262 ATGAAGTGTCTTCTTCTTGGAGTTTACAAGTTATTTCACTTGTAGTCCGGAGATGCAAGTATT 321
|||||
Db 241 atgagaagtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 300
QY 322 CATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAACAGTGTGTTCTTCTTAATGGG 378
|||||
Db 301 catgatacagtagaaaaatctgatcatcctcctagcaaacacagatttcttcttaatggg 357

RESULT 11
US-09-053-375B-1144
; Sequence 1144, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert

Db 121 gccaaactgggtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 180
QY 202 CATATTGATGCTACTTTATATAGCGGAAGTGTATTCACCCCAAGTGTGCAAGGTAACAGCA 261
|||||
Db 181 catattgatgctactttatatacggaaagtgtgttcaccccgagtggttcaccccgagtggttc 240
QY 262 ATGAAGTGTCTTCTTCTTGGAGTTTACAAGTTATTTCACTTGTAGTCCGGAGATGCAAGTATT 321
|||||
Db 241 atgagaagtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 300
QY 322 CATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAACAGTGTGTTCTTCTTAATGGG 379
|||||
Db 301 catgatacagtagaaaaatctgatcatcctcctagcaaacacagatttcttcttaatggga 358

RESULT 10
US-09-442-384B-154
; Sequence 154, Application US/09442384B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashev, Matvey
; TITLE OF INVENTION: Hematology/Immunology Array
; FILE REFERENCE: CLON-006CIP15
; CURRENT APPLICATION NUMBER: US/09/442,384B
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 09/053,375
; PRIOR FILING DATE: 1998-03-31
; NUMBER OF SEQ ID NOS: 830
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleic Acid Probe.
US-09-442-384B-154

Query Match 73.0%; Score 357; DB 5; Length 357;
Best Local Similarity 100.0%; Pred. No. 3.5e-76;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 TTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTTCTTAAACAGTCAATTTCTTAAC 81
|||||
Db 1 ttgagaagtatttccatccagtgctacttggtttacttctaaacagtcattttcttaact 60
QY 82 GAAGCTGGCATTCATCTCTTCTTCTTGGGCTGTTTTCAGTGCAGGGCTTCTTAAACAGAA 141
|||||
Db 61 gaagctggcatttcattctcttcttcttcttcttcttcttcttcttcttcttcttcttctt 120
QY 142 GCCAACTGGGTGAATTAATAGTGAATTTGAAAAAATTTGAAGATCTTATTTCAATCTATG 201
|||||
Db 121 gccaaactgggtgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatgaatga 180
QY 202 CATATTGATGCTACTTTATATAGCGGAAGTGTATTCACCCCAAGTGTGCAAGGTAACAGCA 261
|||||
Db 181 catattgatgctactttatatacggaaagtgtgttcaccccgagtggttcaccccgagtggttc 240
QY 262 ATGAAGTGTCTTCTTCTTGGAGTTTACAAGTTATTTCACTTGTAGTCCGGAGATGCAAGTATT 321
|||||
Db 241 atgagaagtcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 300
QY 322 CATGATACAGTAGAAAAATCTGATCATCTAGCAAAACAAACAGTGTGTTCTTCTTAATGGG 378
|||||
Db 301 catgatacagtagaaaaatctgatcatcctcctagcaaacacagatttcttcttaatggg 357

RESULT 11
US-09-053-375B-1144
; Sequence 1144, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert

```

: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 1144
: LENGTH: 1250
: TYPE: DNA
: ORGANISM: Mus musculus
: US-09-053-375B-1144

```

Query Match	68.9%	Score	337	DB	5	Length	1250
Best Local Similarity	80.6%	Pred.	No. 2.8e-71				
Matches	394	Conservative	0	Mismatches	95	Indels	0
							Gaps
QY	1	ATGGAATTTTCGAACACACATTTCAGAAAGTATTTCCATCCAGTCTACTGTGTTTACTT	60				
Db	466	atgaaatttgaaacacatatagaggaaacacatcccatctgctactgtgttccct	525				
QY	61	CTAAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTCATTTGGGCTGTTTCAGT	120				
Db	526	ctaaacagtcacattttaaactgaggctggtcattcatcttccatttgggctgctcagt	585				
QY	121	GCAGGGCTTCCTTAAACAGAGCCAACTGGGTGAATTAATAAGTGTATTTCAAAAAAATT	180				
Db	586	gtgggtctccctaaacagagggccactggtatagatgtaagatatgacctggagaaatt	645				
QY	181	GAGATCTTATTCAACTATGTCATATTGATGCTACTTTATACGGAAAGTGATGTTTCAAC	240				
Db	646	gaaagccttattcaactattcatattgacaccactttacactgcagtgactttccat	705				
QY	241	CCCAGTGTCAAAAGTAAACAGCAATGAAGTGTCTTCTCTTGGAGTTACAAAGTTATTTCACTT	300				
Db	706	ccagttgcaagttactgctgcaatgaaactgtcttccctggaaatgcagggttatttcaat	765				
QY	301	GAGTCCGGAGATCGAAGTATTTCATGATACAGTAAAGAAATCTGATCATCTAGCAAAACAC	360				
Db	766	gagtcagtaacatgactctttaatgaaacagtaagaaacgtgctctaccttgcaaacagc	825				
QY	361	AGTTTGTCTTCTAATGGGATGTAACAGATCTGGATGCGAAAGATCTGAGGAACACTGGAG	420				
Db	826	acctgtcttctaacgaagaatgtagcagaatctggtgctgcaaggaatgtaggagctggag	885				
QY	421	GA AAAAATAATTAAGAAATTTTTCACAGATTTTGTACATATTGTCCAAATGTTTCATCAAC	480				
Db	886	gagaaacaccttcacagagtttttgcaaaagctttatacagcattgtccaaatgtttcatcaac	945				
QY	481	ACTTCTTGA	489				
Db	946	acctctctga	954				

```

RESULT 12
US-10-191-803-72
: Sequence 72, Application US/10191803
: GENERAL INFORMATION:
: APPLICANT: MENDRICK, Donna
: APPLICANT: PORTER, Mark
: APPLICANT: JOHNSON, Kory
: APPLICANT: HIGGS, Brandon
: APPLICANT: CASTLE, Arthur
: APPLICANT: ELASHOFF, Michael
: TITLE OF INVENTION: Cardiotoxin Molecular
: FILE REFERENCE: 44921-5090US
: CURRENT APPLICATION NUMBER: US/10/191-803
: CURRENT FILING DATE: 2002-07-10
: PRIOR APPLICATION NUMBER: US 60/303,819
: PRIOR FILING DATE: 2001-07-10
: PRIOR APPLICATION NUMBER: US 60/305,623
: PRIOR FILING DATE: 2001-07-17
: PRIOR APPLICATION NUMBER: US 60/369,351

```

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; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 1313
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_013129
US-10-191-803-72

```

Query Match	67.9%;	Score 332.2;	DB 6;	Length 1313;
Best Local Similarity	80.0%;	Pred. No. 4e-70;		
Matches 391;	Conservative 0;	Mismatches 98;	Indels 0;	Gaps
QY 1	ATGAGAAATTCGAAACACCAATTTGAGAAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT	60		
Db 546	atgaaaatTTgaaacacatagatgaggaatacatccatcttctgtactactctgtgttccct	605		
QY 61	CTAAACAGATCATTTTTCTAACTGAAGCTGGCAATTCATGCTTTCATTTTGGGTGGTTTCAGT	120		
Db 606	ctcaacagtcactctttaactgaggctggcagtcaccatgctcttcattttgggctgtgtcagt	665		
QY 121	GCAGGGCTTCCTAAAACAGAACCAACTCGGTGCAATTAAGTGAATTTGAAAAAAATTT	180		
Db 666	gtaggctctccctaaacacagaggccaactgtagatgtaagatcacagctcgagagaaatt	725		
QY 181	GAGATCTTATTCAAATCTATGCTATATTGATGTACTCTTTATATACGGAAGTGTGTTCCAC	240		
Db 726	gaaagctctattcaatttattcatattgatactactatcacactgcagctgactttcat	785		
QY 241	CCCAGTTGCAAAAGTAAACAGCAATGAAGTGCTTCTCTTGGAGTTACAAGTTTATTTTCATT	300		
Db 786	cccagttgcaagttactgccaatgaaactgctttctctcctggaaattacacaggttatitttgcac	845		
QY 301	GAGTCGGAGATGCAAGTATTCATGATACAGTAGAAAATCTGATCATCCTAGCAAAACAC	360		
Db 846	gagtcagtaaacatgactcttaatgaaacagtaagaaacgtgctctactcttgcgaacagc	905		
QY 361	AGTTTCTCTCTAATGGGAATCTAACAGNATCTGATGCAAGATGTGAGGAACCTGGAG	420		
Db 906	accctgtctcttaaacagaagaatgtaatatgctgtggtcgaaggaaatgtcgaggagctggag	965		
QY 421	GAAGAAAAATTTAAAGAAATTTTTCGAGAGTTTGTGTACATATTTGCCAAATGTTTCATCAAC	480		
Db 966	gagagaaactcacggagtttttgcagagttttatacatattgtccaaatgttccatcaac	1025		
QY 481	ACTTCTTTGA 489			
Db 1026	acgtctgta 1034			

```

RESULT 13
US-09-454-226A-527
; Sequence 527, Application US/09454226A
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Lukashyev, Matvey
; TITLE OF INVENTION: Rat Array
; FILE REFERENCE: CLON-006CIP12
; CURRENT APPLICATION NUMBER: US/09/454, 226A
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 1186
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 527
; LENGTH: 285
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized gene fragment

```


US-09-454-226A-527

Query Match	32.3%	Score 157.8;	DB 5;	Length 285;
Best Local Similarity	78.4%;	Pred. No. 2e-28;		
Matches 189;	Conservative	0;	Mismatches 52;	Indels 0;
Gaps 0;				

Qy	249	C A A A G T A C A C G C A A T G A A G T G C T T C T C T T G G A G T T A C A A G T A T T T C A C T T G A G T C C G G	308
D b	1	c a a g t t a c t g c a a t g a a c t g t t c t c t g a a t t a c a g g t t a t t t g c a g a g t a c a g	60
Qy	309	A G A T G C A A G T A T T C A T G A C A C T A C A A A T C T G A T C A C C T A G C A A A C A A C A G T T T G P C	368
D b	61	t a a c a t g a c t c t t a a g a a a c a g t a a g a a a c g t g t c t a c c t t g a a a c a g a c a c t g t c	120
Qy	369	T T C T A T T G G A A T G T T A C A G A A T C T G G A T G C A A A G A A T G T G A G G A A C T G G A G G A A A A A A	428
D b	121	t t c t a c a a g a a t g t a a t a g a g c t g c t g c a a g g a a t g t g a g g a g c t g g a g g a g a g a a	180
Qy	429	T A T T A A G A A T T T T G C A G A G T T T T C T A C A T A T T G C C A A A T G T T C A T C A T C A A C A C T T C T T G	488
D b	181	c t c a g g a g t t t t g c a g a g t t t t a t a t a t t g t c c a a a t g t t c c a t c a a c a c g t c c t g	240
Qy	489	A 489 	
D b	241	a 241	

RESULT 14

US-10-216-086-422 ; Sequence 422, Application US/10216086

```

: GENERAL INFORMATION:
: APPLICANT: RQbison, Keith
: TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
: FILE REFERENCE: 5800-57
: CURRENT APPLICATION NUMBER: US/10/216,086
: CURRENT FILING DATE: 2002-08-09
: PRIOR APPLICATION NUMBER: US/09/419,553
: PRIOR FILING DATE: 1999-10-15
: NUMBER OF SEQ ID NOS: 725
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 422
:

```

```

: LENGTH: 181
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (0)..(0)
: OTHER INFORMATION: mining entry:13176
US-10-216-086-422

```

Query Match	23.7%	Score 116;	DB 6;	Length 181;
Best Local Similarity	77.8%	Pred. No. 1.9e-18;		
Matches 140;	Conservative	0;	Mismatches 40;	Indels 0;
Gaps 0;				

Qy	3	GAGAAATTCGAACACATTTGAGAGTATTTCCATCCAGTCTACTGTGTTTACTTCT	62
Db	1	gagaatttcggaacaaaaattgagaagtaattccattcagtggaattggttacttcc	60
Qy	63	AACAGTCAATTTCTTACTGACGTGGCAATCATGTCTTCAATTTGGGCTGTTTCAGTGC	122
Db	61	aaacagtcgaattcctaattgagcttggaaatcaaggctccatttgggtggttcagttc	120
Qy	123	AGGCTTCCTTAAACAGAACCCAACTGGGTGAATGTAAATAGTGATTTCAAAAAATTTGA	182
Db	121	aagggttctcaaaagaagcgaatgggttgatgcaataaagtgattgaaaaattta	180

RESULT 15

US-10-106-698-2528 ; Sequence 2528, Application US/10106698

; GENERAL INFORMATION:

```

: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypept
: FILE REFERENCE: PA005PI
: CURRENT APPLICATION NUMBER: US/10/106,698
: CURRENT FILING DATE: 2002-03-27
: PRIOR APPLICATION NUMBER: PCT/US00/26524
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: US 60/157,137
: PRIOR FILING DATE: 1999-09-29
: PRIOR APPLICATION NUMBER: US 60/163,280
: PRIOR FILING DATE: 1999-11-03
: NUMBER OF SEQ ID NOS: 8564
: SOFTWARE: PatentIn Ver. 3.0
: SEQ ID NO 2528
: LENGTH: 565
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (4)..(4)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (45)..(45)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (125)..(125)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (149)..(149)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (212)..(212)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (216)..(216)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (260)..(260)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (294)..(294)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (298)..(298)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (305)..(305)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (312)..(312)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (462)..(462)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (495)..(495)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (497)..(497)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (542)..(542)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (547)..(547)
: OTHER INFORMATION: n equals a,t,g, or c
: NAME/KEY: misc_feature
: LOCATION: (552)..(552)
: OTHER INFORMATION: n equals a,t,g, or c
: US-10-106-698-2528

```

Query Match

21.08; Score 102.6; DB 7; Length 565;

Best Local Similarity 83.0%; Pred. No. 3.8e-15;
Matches 220; Conservative 0; Mismatches 32; Indels 13; Gaps 9;

Qy	1	ATGAGATTTCGAAACACACATTT--GAGAAGTATTTCCAT-CCAGTGTCTACTTTGTGTTTA	57
Db	301	atganaatttcnaaacacacattttgaaaaattatttccatccccagtgctacttggttta	360
Qy	58	CTTCTAAACAGTCATTTTCTAACT--GAAGCTGGCATT-CATGCTTCA-TTTTGGGCTG	113
Db	361	cttcttaacaatcatttctaacttgaagctggcattccatgtcttcatttttgggctg	420
Qy	114	TTTCAGTGCA--GGCTTCCTAAACACAGCCAACTGGGTGAATG-TAATAAGTCATTT	170
Db	421	tttcaatgcaagggttcctctaaacaaacaaactgggnaatgtttattaaagtattt	480
Qy	171	GAATAAAATT-GAAGATCTTATTAATCATGCTATTTGATGCTACTTTATATAC--GGA	227
Db	481	gaaaaaaatttggaananatttccatctatgccttttgatgctactttattccggaa	540
Qy	228	AAGTGATGTTCAACCCAGTTGCAA	252
Db	541	anttaanttcnccccattttccaa	565

Search completed: September 20, 2002, 00:17:37
Job time: 5302 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:25:50 ; Search time 1845.14 Seconds
(without alignments)
5545.962 Million cell updates/sec

Title: US-09-196-427-2

Perfect score: 489

Sequence: 1 ATGAGAAATTCGAACACCA.....TGTTTCATCACACTTCTTGA 489

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.htg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.om.*

21: em.or.*

22: em.ov.*

23: em.pat.*

24: em.ph.*

25: em.pl.*

26: em.ro.*

27: em.sts.*

28: em.un.*

29: em.vi.*

30: em.htg.hum.*

31: em.htg_inv.*

32: em.htg_other.*

33: em.htg_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
------------	-------	-------	--------	-------	-------------

1	489	100.0	489	6	AR004268	AR004268 Sequence
2	489	100.0	489	6	AR024349	AR024349 Sequence
3	489	100.0	489	6	AR070281	AR070281 Sequence
4	489	100.0	489	6	AR085740	AR085740 Sequence
5	489	100.0	489	6	AR122046	AR122046 Sequence
6	489	100.0	489	6	AR122868	AR122868 Sequence
7	489	100.0	489	6	AR125105	AR125105 Sequence
8	489	100.0	489	6	AX006786	AX006786 Sequence
9	489	100.0	489	6	AX320244	AX320244 Sequence
10	489	100.0	489	6	I25783	I25783 Sequence 4
11	489	100.0	489	6	I28849	I28849 Sequence 1
12	489	100.0	489	6	I62692	I62692 Sequence 1
13	489	100.0	489	6	I79219	I79219 Sequence 1
14	489	100.0	1202	6	AR103280	AR103280 Sequence
15	489	100.0	1202	6	AX024715	AX024715 Sequence
16	489	100.0	1202	6	AX301227	AX301227 Sequence
17	489	100.0	1202	9	HSU14407	U14407 Human Inter
18	487.4	99.7	489	6	AR094649	AR094649 Sequence
19	487.4	99.7	489	6	BD008811	BD008811 Antagonis
20	482.6	98.7	489	6	AX320242	AX320242 Sequence
21	481	98.4	489	6	AR094650	AR094650 Sequence
22	481	98.4	489	6	BD008812	BD008812 Antagonis
23	466.6	95.4	492	9	AB000555	AB000555 Macaca fa
24	466.6	95.4	559	9	MMU19843	U19843 Macaca mula
25	465	95.1	489	6	AR004267	AR004267 Sequence
26	465	95.1	489	6	AR024348	AR024348 Sequence
27	465	95.1	489	6	AR070282	AR070282 Sequence
28	465	95.1	489	6	AR085741	AR085741 Sequence
29	465	95.1	489	6	AR122045	AR122045 Sequence
30	465	95.1	489	6	AR122867	AR122867 Sequence
31	465	95.1	489	6	AR125104	AR125104 Sequence
32	465	95.1	489	6	AX006785	AX006785 Sequence
33	465	95.1	489	6	I25782	I25782 Sequence 1
34	465	95.1	489	6	I28850	I28850 Sequence 4
35	465	95.1	489	6	I79220	I79220 Sequence 4
36	465	95.1	1275	9	CAU03099	U03099 Cercopithec
37	451.4	92.3	453	9	HSIL15MR	238000 H.sapiens m
38	394.6	80.7	489	4	BTU42433	U42433 Bos taurus
39	386.6	79.1	489	4	AFI08148	AFI08148 Felis cat
40	386.6	79.1	489	4	SSU58142	U58142 Sus scrofa
41	380	77.7	643	9	HSIL15MR1	X94222 H.sapiens m
42	380	77.7	643	9	HSIL15MR2	X94223 H.sapiens m
43	378.6	77.4	489	4	AFI49700	AFI49700 Ovis arie
44	378.4	77.4	1248	6	AR087004	AR087004 Sequence
45	378.4	77.4	1248	9	AF031167	AF031167 Homo sapi

ALIGNMENTS

RESULT	1					
AR004268						
LOCUS	AR004268	489 bp	DNA	linear	PAT 04-DEC-1998	
DEFINITION	Sequence	4	from patent US 5747024.			
ACCESSION	AR004268					
VERSION	AR004268.1	GI:3965147				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 489)					
AUTHORS	Grabstein,K.H. and Widmer,M.B.					
TITLE	Vaccine adjuvant comprising interleukin-15					
JOURNAL	Patent: US 5747024-A 4 05-MAY-1998;					
FEATURES	Location/Qualifiers					
source	1..489					
BASE COUNT	159 a	79 c	95 g	156 t		
ORIGIN	/organism="unknown"					

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;

	Query Match	100.0%;	Score 489;	DB 6;	Length 489;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-92;		
	Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATCAGAAATTTCGAAACCAATTTGAGAAGTATTTCCATCCAGTGCCTACTGCTGTTTACTT	60		
Db	1	ATGAGAATTTCGAAACCAATTTGAGAAGTATTTCCATCCAGTGCCTACTGCTGTTTACTT	60		
QY	61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGCTTTCAGT	120		
Db	61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTGGGCTGCTTTCAGT	120		
QY	121	GCAGGGCTTCCTAAAACAGAAGCAACTGGGTGAATGTAATAAGTGAATTTGAAAAAAATT	180		

Query Match	100.0%;	Score 489;	DB 6;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 1.2e-92;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	ATGAGAATTTGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTCACTT	60		
Db 1	ATGAGAATTTGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTCACTT	60		
QY 61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTTGGCGCTGTTTCAGT	120		
Db 61	CTAAACAGTCATTTTCTTAAGTGAAGCTGGCATTCATGCTCTTCATTTTGGCGCTGTTTCAGT	120		
QY 121	GCAGGGCTTCCTAAACACAGAACCACTGGGTGAATGTATTAAGTGCATTTGAAAAAAATTT	180		
Db 121	GCAGGGCTTCCTAAACACAGAACCACTGGGTGAATGTATTAAGTGCATTTGAAAAAAATTT	180		
QY 181	GAAGATCTTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAAGTGATGTTTCAC	240		
Db 181	GAAGATCTTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAAGTGATGTTTCAC	240		
QY 241	CCAGTTGCAAGTACACGAATGAAGTGGTTCCTCTTGGAGTTACAAGTTAATTCACATT	300		
Db 241	CCAGTTGCAAGTACACGAATGAAGTGGTTCCTCTTGGAGTTACAAGTTAATTCACATT	300		

Query Match	100.0%;	Score 489;	DB 6;	Length 489;
Best Local Similarity	100.0%;	Pred. No. 1.2e-92;		
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGAGAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTACTT	60	
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QY	61	CTAAACAGTCATTTCTTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGCTTTCAGT	120	
Db	61	CTAAACAGTCATTTCTTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGCTTTCAGT	120	
QY	121	GCAGGGTCTCTAAACACAGAGCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAAT	180	
Db	121	GCAGGGTCTCTAAACACAGAGCCACTGGGTGAATGTAATAAGTGATTTGAAAAAAAT	180	
QY	181	GAAGATCTTATTCAAATCTATGCATATTTGATGCTACTTTATATACGAAAGTGAATTCAC	240	
Db	181	GAAGATCTTATTCAAATCTATGCATATTTGATGCTACTTTATATACGAAAGTGAATTCAC	240	
QY	241	CCAGTTGCCAAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTATTATTCAC	300	
Db	241	CCAGTTGCCAAAGTAACAGCAATGAAGTGCTTTCTCTTGGAGTTACAAGTATTATTCAC	300	

QY 301 GAGTCGGAGATCAAGTATTCATGATACAGTAGAGAAAATCTGATCATCTAGCAAAACAC 360
Db 301 GAGTCGGAGATCAAGTATTCATGATACAGTAGAGAAAATCTGATCATCTAGCAAAACAC 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
RESULT 4
LOCUS AR085740 489 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from patent US 5985262.
ACCESSION AR085740
VERSION AR085740.1 GI:10012506
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Method of treatment with epithelium derived T-cell factor
JOURNAL Patent: US 5985262-A 1 16-NOV-1999;
FEATURES Location/Qualifiers
source
i. .489
/organism="unknown"
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 GCAGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
Db 121 GCAGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAAGTGAATTTGAAAAAAT 180
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Db 181 GAAGATCTTATCAATCTATGATATTCATGCTACTTTATATACGGAAGTGTGTTTCAAC 240
QY 241 CCAGTTGCAAAAGTAAACAGCAATGAAGTGTCTTCTTGGAGTTACAAATTTTTCAC 300
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QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480

QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
RESULT 5
LOCUS AR122046 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6165466.
ACCESSION AR122046
VERSION AR122046.1 GI:14106363
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.
TITLE Antagonists of interleukin-15
JOURNAL Patent: US 6165466-A 2 26-DEC-2000;
FEATURES Location/Qualifiers
source
i. .489
/organism="unknown"
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60
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QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATGTGAGGAATGGAG 420
QY 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATATTAAAGAAATTTTGGCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
RESULT 6
LOCUS AR122868 489 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 2 from patent US 6168783.
ACCESSION AR122868

VERSION ARI22868.1 GI:14107834

KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of interleukin-15

JOURNAL Patent: US 6168783-A 2 02-JAN-2001;

FEATURES Location/Qualifiers

source 1. 489

BASE COUNT 159 a 79 c 95 g 156 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.2e-92;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGAGAAATTCGAAACCCACATTTGAGAAGTATTCCATCCAGTGTCTTCTTGGGCTGTTTCACTT 60

QY 61 CTAACAGTCATTTCTACTGAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCACTT 120

Db 61 CTAACAGTCATTTCTACTGAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCACTT 120

QY 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATGAAGTATTGAAAAAATTT 180

Db 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATGAAGTATTGAAAAAATTT 180

QY 181 GAAGATCTTATTCAATCTATGTCATATTCATGCTCTTCTTGGGCTGTTTCACTT 240

Db 181 GAAGATCTTATTCAATCTATGTCATATTCATGCTCTTCTTGGGCTGTTTCACTT 240

QY 241 CCCAGTTCGAAAGTACAGCAATGAAGTCTTCTTCTTGGGCTGTTTCACTT 300

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QY 301 GAGTCGGAGATGCAAGTATTCTATGATACAGTGTCTTCTTGGGCTGTTTCACTT 360

Db 301 GAGTCGGAGATGCAAGTATTCTATGATACAGTGTCTTCTTGGGCTGTTTCACTT 360

QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAATGTGAGGAATGGGAG 420

Db 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAATGTGAGGAATGGGAG 420

QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480

Db 421 GAAAAAATATTAAAGAAATTTTTCAGAGATTTTGTACATATTGTCCAAATGTTTCATCAAC 480

QY 481 ACTTCTTGA 489

Db 481 ACTTCTTGA 489

RESULT 7

LOCUS ARI25105 489 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 2 from patent US 6177079.

ACCESSION ARI25105

VERSION ARI25105.1 GI:14111167

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 489)

AUTHORS Grabstein,K.H., Pettit,D.K. and Paxton,R.J.

TITLE Antagonists of interleukin-15

JOURNAL Patent: US 6177079-A 2 23-JAN-2001;

FEATURES Location/Qualifiers

source 1. 489

BASE COUNT 159 a 79 c 95 g 156 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.2e-92;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTTCTTGA 489

Db 481 ACTTCTTGA 489

RESULT 8

LOCUS AX006786 489 bp DNA linear PAT 06-SEP-2000

DEFINITION Sequence 4 from Patent WO0002582.

ACCESSION AX006786

VERSION AX006786.1 GI:9994822

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 489)

AUTHORS Londel,M., Quarantino,S. and Maiuri,L.

TITLE Treatment of celiac disease with interleukin-15 antagonists

JOURNAL Patent: WO 0002582-A 4 20-JAN-2000;

FEATURES Location/Qualifiers

source 1. 489

BASE COUNT 159 a 79 c 95 g 156 t

ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;

Best Local Similarity 100.0%; Pred. No. 1.2e-92;

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Db 61 CTAACAGTCATTTTCTAACTCAAGCTGGCATTCATGCTTCTTCAATTTGGGCTGTTCAGT 120
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Db 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTCAACAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 9
AX320244
LOCUS AX320244 489 bp DNA linear PAT 14-DEC-2001
DEFINITION Sequence 3 from Patent WO0187330.
ACCESSION AX320244
VERSION AX320244.1 GI:17901652
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (sites)
REFERENCE Strom,T.B. and Maslinski,W.
AUTHORS Compositions and methods for achieving immune suppression
TITLE Patent: WO 0187330-A 3 22-NOV-2001;
JOURNAL Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES
source
1..489
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 489; DB 6; Length 489;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 1.2e-92;
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Db 361 AGTTGTCTTCTTAATGGGAATGTAACAGATCTGGATGCAAAAGATGTGAGGAAGTGGAG 420
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTCAACAAC 480
Db 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTCAACAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 10
I25783
LOCUS I25783 489 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 4 from patent US 5552303.
ACCESSION I25783
VERSION I25783.1 GI:1605653
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K., Anderson,D., Eisenman,J., Fung,V. and Rauch,C.
TITLE DNA encoding epithelium-derived T-cell factor
JOURNAL Patent: US 5552303-A 4 03-SEP-1996;
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BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match
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QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
RESULT 11
LOCUS I28849 489 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5574138.
ACCESSION I28849
VERSION I28849.1 GI:1819629
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung,V. and Rauch,C.
TITLE Epithelium-derived T-cell factor
JOURNAL Patent: US 5574138-A 1 12-NOV-1996;
FEATURES Location/Qualifiers
source
1. 489
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGAATTTTCGAAACCACTTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTTACTT 60
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QY 181 GAAGATCTTATTCAATCTATGATATGATGCTACTTTATATACGGAAGTGAATTTTCACTT 240
Db 181 GAAGATCTTATTCAATCTATGATATGATGCTACTTTATATACGGAAGTGAATTTTCACTT 240
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Db 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTGACATATTTGTCCTCAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489
RESULT 12
LOCUS I62692 489 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5660824.
ACCESSION I62692
VERSION I62692.1 GI:2480400
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 489)
AUTHORS Grabstein,K.H., Quinn,L.S. and Troutt,A.B.
TITLE Muscle trophic factor
JOURNAL Patent: US 5660824-A 1 26-AUG-1997;
FEATURES Location/Qualifiers
source
1. 489
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ORIGIN
Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 481 ACTTCTTGA 489

RESULT 13

LOCUS I79219

DEFINITION Sequence 1 from patent US 5707616. 489 bp DNA linear PAT 10-JUN-1998

ACCESSION I79219

VERSION I79219.1 GI:3207509

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 489)
Grabstein,K.H., Anderson,D.M., Eisenman,J.R., Fung V. and Rauch,C.
TITLE Method for treating or preventing gastrointestinal disease with
epithelium-derived T-cell factor
JOURNAL Patent: US 5707616-A 1 13-JAN-1998;
FEATURES Location/Qualifiers
source 1..489
BASE COUNT 159 a 79 c 95 g 156 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.2e-92;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCATCCAGTCTACTTGTGTTTACTT 60
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Db 1 ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCATCCAGTCTACTTGTGTTTACTT 60
|||||

QY 61 CTAACAGTCAATTTCTTAAGCTGAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
|||||

Db 61 CTAACAGTCAATTTCTTAAGCTGAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
|||||

QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT 180
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Db 121 GCAGGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT 180
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QY 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGGAAGTGAATGTTTCAC 240
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Db 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGGAAGTGAATGTTTCAC 240
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QY 241 CCCAGTGCAGAGTCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 300
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Db 241 CCCAGTGCAGAGTCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 360
|||||

Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 360
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QY 361 AGTTGTCCTTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
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Db 361 AGTTGTCCTTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
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QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
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Db 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
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Db 481 ACTTCTTGA 489

RESULT 14

LOCUS AR103280

DEFINITION Sequence 1 from Patent WO028019. 1202 bp DNA linear PAT 15-SEP-2000

ACCESSION AR103280

VERSION AR103280.1 GI:10184794

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1202)
AUTHORS Douddevani,A. and Chaimovitz,C.
TITLE Antisense oligomer

DEFINITION Sequence 11 from patent US 6087172.

ACCESSION AR103280

VERSION AR103280.1 GI:12814868

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1202)
Veerapaneni,D., Hamanaka,S. and Nozawa,I.
TITLE Ribozymes targeted to human IL-15 mRNA
JOURNAL Patent: US 6087172-A 11 11-JUL-2000;
FEATURES Location/Qualifiers
source 1..1202
BASE COUNT 355 a 219 c 249 g 379 t
ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;
Best Local Similarity 100.0%; Pred. No. 9.4e-93;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCATCCAGTCTACTTGTGTTTACTT 60
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Db 317 ATGAGAAATTCGAAACCCACATTTTCCAGAGTATTTCATCCAGTCTACTTGTGTTTACTT 376
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QY 61 CTAACAGTCAATTTCTTAAGCTGAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
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Db 377 CTAACAGTCAATTTCTTAAGCTGAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 436
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QY 121 GCAGGGCTTCTTAAACAGAGCCAACTGGTGAATGTAATAGTGAATTTGAAAAAATTT 180
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QY 181 GAAGATCTTATTCATCTATGATGCTACTTATATACGGAAGTGAATGTTTCAC 240
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QY 241 CCCAGTGCAGAGTCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTGAAGTCTTCTCTTGGAGTTACAGTTATTTCACTT 360
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QY 361 AGTTGTCCTTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
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Db 677 AGTTGTCCTTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAACCTGGAG 736
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QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
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Db 737 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 796
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QY 481 ACTTCTTGA 489
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Db 797 ACTTCTTGA 805

RESULT 15

LOCUS AX024715

DEFINITION Sequence 1 from Patent WO028019. 1202 bp DNA linear PAT 15-SEP-2000

ACCESSION AX024715

VERSION AX024715.1 GI:10184794

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1202)
AUTHORS Douddevani,A. and Chaimovitz,C.
TITLE Antisense oligomer

JOURNAL Patent: WO 0028019-A 1 18-MAY-2000;
 MOR RESEARCH APPLIC LTD (IL) ; DOUDEVANI AMOS (IL) ; UNIV BEN
 GURION (IL) ; CHAIMOVITZ CIDIO (IL)
 FEATURES Location/Qualifiers
 source 1..1202
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 355 a 219 c 249 g 379 t
 ORIGIN

Query Match 100.0%; Score 489; DB 6; Length 1202;
 Best Local Similarity 100.0%; Pred. No. 9.4e-93;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACACATTGAGAAGTATTTCATCCAGTGGCTACTTGTGTTTACTT 60
 Db 317 ATCAGAAATTCGAAACACACATTGAGAAGTATTTCATCCAGTGGCTACTTGTGTTTACTT 376

QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCACT 120
 Db 377 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCACT 436

QY 121 GCAGGGCTTCCTAAACAGACGCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 180
 Db 437 GCAGGGCTTCCTAAACAGACGCCAACTGGGTGAATGTAATAGTCAATTTGAAAAAATT 496

QY 181 GAAGATCTTATTCAATCTATGATATGATGCTACTTTATATACGGAAGTGTGTTTCACT 240
 Db 497 GAAGATCTTATTCAATCTATGATATGATGCTACTTTATATACGGAAGTGTGTTTCACT 556

QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACTT 300
 Db 557 CCCAGTTGCAAAAGTAACAGCAATGAAGTCTTCTCTGGAGTTACAAAGTTATTTCACTT 616

QY 301 GAGTCGGGAGATGCAAGTATTTCATGATCAGTAGAATACTCATCATCTAGCAAAACAAC 360
 Db 617 GAGTCGGGAGATGCAAGTATTTCATGATCAGTAGAATACTCATCATCTAGCAAAACAAC 676

QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAAGTGGAG 420
 Db 677 AGTTTGTCTTCTTAATGGGAATGTAACAGAACTGGATGCAAGAAATGTGAGGAAGTGGAG 736

QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCAATCAAC 480
 Db 737 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTACATATTGTCCAAATGTTTCAATCAAC 796

QY 481 ACTTCTTGA 489
 Db 797 ACTTCTTGA 805

Search completed: September 19, 2002, 23:20:16
 Job time: 10466 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 22:10:00 ; Search time 200.5 Seconds
(without alignments)
4187.387 Million cell updates/sec

Title: US-09-196-427-2
Perfect score: 489
Sequence: 1 ATCAGAAATTCGAACACACA.....TGTCATCAACACTTCTGA 489

Scoring table:

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	100.0	489	16 AAT00526	Human interleukin-
2	489	100.0	489	16 AAT04584	Human IL-15 clone
3	489	100.0	489	17 AAT49455	Human epithelium
4	489	100.0	489	17 AAT42243	Human epithelium-d
5	489	100.0	489	17 AAT36635	Human interleukin-
6	489	100.0	489	18 AAT58404	Interleukin-15 cod
7	489	100.0	489	19 AAV23554	Human interleukin-
8	489	100.0	489	19 AAV02873	Simian epithelium
9	489	100.0	489	20 AAX29479	Simian epithelium-

10	489	100.0	489	21 AAZ90032	Human interleukin-
11	489	100.0	489	21 AAZ38244	Simian epithelium-
12	489	100.0	489	22 AAD14465	Human interleukin
13	489	100.0	489	22 AAF57017	Simian ETF (SETF)
14	489	100.0	1202	20 AAX56368	Human IL-15 DNA
15	489	100.0	1202	21 AAF21342	Human low adenosin
16	489	100.0	1202	21 AAX58044	Human interleukin-
17	489	100.0	1202	21 AAX35220	Human adenosine re
18	489	100.0	1202	21 AAZ88708	Human IL-15 cDNA
19	489	100.0	17904	21 AAF21345	Human low adenosin
20	487.4	99.7	489	18 AAT97227	Wild-type interleu
21	481	98.4	489	18 AAT97228	Mutant interleukin
22	465	95.1	489	16 AAT00524	Simian interleukin
23	465	95.1	489	16 AAX84583	Simian IL-15 clone
24	465	95.1	489	17 AAT49456	Human epithelium d
25	465	95.1	489	17 AAT42242	Simian epithelium-
26	465	95.1	489	17 AAT36634	Simian interleukin-
27	465	95.1	489	19 AAV02874	Human epithelium d
28	465	95.1	489	20 AAX29480	Human epithelium-d
29	465	95.1	489	21 AAZ90031	Simian interleukin
30	465	95.1	489	21 AAZ38245	Human epithelium-d
31	465	95.1	489	22 AAF57018	Human ETF (hETF) p
32	385	78.7	17844	21 AAX35223	Human adenosine re
33	378.4	77.4	1248	21 AAF21341	Human low adenosin
34	378.4	77.4	1248	21 AAX35219	Human adenosine re
35	378.4	77.4	1248	21 AAZ37358	Human interleukin-
36	351.6	71.9	486	21 AAF21344	Human low adenosin
37	351.6	71.9	486	21 AAX35222	Human adenosine re
38	345	70.6	345	16 AAT00527	Human interleukin-
39	345	70.6	345	22 AAF57024	Simian ETF (SETF)
40	325.8	66.6	345	16 AAT00525	Simian interleukin
41	325.8	66.6	345	22 AAF57025	Human ETF (hETF) m
42	141.6	29.0	14968	21 AAF21343	Human low adenosin
43	141.6	29.0	14968	21 AAX35221	Human adenosine re
44	141.6	29.0	14968	22 AAD14464	Human IL-15 gene a
45	141.6	29.0	14968	22 AAD15838	Human interleukin

ALIGNMENTS

RESULT 1
AAT00526
ID AAT00526 standard; cDNA; 489 BP.

XX AC AAT00526;

XX DT 02-FEB-1996 (first entry)

XX DE Human interleukin-15 precursor.

XX KW Interleukin-15; epithelium-derived T-cell factor; T lymphocyte; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX CDS 1..489

XX FT /tag= a

XX FT /note= "claimed"

XX FT misc_feature 145..489

XX FT /tag= b

XX FT /note= "claimed"

XX PN WO9527722-A.

XX PD 19-OCT-1995.

XX PF 06-APR-1994; 94WO-US03793.

XX PR 06-APR-1994; 94WO-US03793.

XX PA (IMV) IMMUNEX CORP.

PI Anderson DM, Eisenman JR, Fung V, Grabstein KH;
 PI Rauch C;

DR WPI; 1995-373556/48.
 DR P-PSDB; AAR83438.

PT Isolated DNA encoding polypeptide with mammalian IL-15 activity - which
 PT stimulates proliferation and differentiation of T cells, used for
 PT treating carcinoma(s), melanomas, etc. and viral infections
 XX
 PS Claim 36; Page 28-29; 48pp; English.

CC A simian species of IL-15 (sIL-15) was purified and its AA
 CC sequence and cDNA sequence analysed (see AAR83309, AAR83436,
 CC AAR00524, AAR00525). Both the simian and the human ORFs encode
 CC a precursor polypeptide (AAR83436, AAR83438). The precursor
 CC polypeptides each comprise a 48-AA leader sequence and a sequence
 CC encoding mature simian or human IL-15 polypeptides. The active
 CC simian and human IL-15 polypeptides are disclosed in AAR83309 &
 CC AAR83310 respectively. The invention also comprises other mammalian
 CC IL-15, including human IL-15, that hybridise to probes defined by
 CC AAR83438. A plasmid contg. a recombinant clone of human IL-15
 CC cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245.
 CC The deposit was named 141-hETF. AAR83435 is a mammalian mature
 CC IL-15 polypeptide. It is a generic sequence which encompasses both
 CC AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.

XX
 SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60
 Db 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctacttgtgttactt 60
 QY 61 CTAACAGCTCAATTTCTTAACAGCTGGCATTCATGTCCTTCAATTTGGGCTGTTCACT 120
 Db 61 cttaacagctcattttcttaactgaagctggcattcattcttcttcttcttcttcttctt 120
 QY 121 GCAGGGCTTCTAAACAGAACGCACTGGTGAATGTAATAGTATTTGAAAAAATT 180
 Db 121 gcagggtcttctaaacagaaacagcaactgggtgaatgtaataagtatttgaaaaaatt 180
 QY 181 GAAGATCTTATTCATCTATGCTATGCTACTTTATATACGGAAGTGTGTTTCAAC 240
 Db 181 gaagatcttattcaatctatgcatattgacttactttatatatacggaaagtgtgttcaac 240
 QY 241 CCCAGTTCGAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAGTTTATTTCACTT 300
 Db 241 cccagttgcaagtaaacagcaatgaagtgcttcttcttcttcttcttcttcttcttctt 300
 QY 301 GAGTCCGAGATGCAAGTATTCATGATACATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 gagtccgagatgcaagtatttcattgatacagatacagatacagatacagatacagatacag 360
 QY 361 AGTTTGTCTTCTAATGGAATGTAACAGAAATCTGGATGCAAGAAATGTAAGAAATCTGGAG 420
 Db 361 agtttgtcttcttaatggaatgtaacagaaatctggatgcaagaaatgtaagaaatctggag 420
 QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTGTACATATTTGTCGAAATGTTTCATCAAC 480
 Db 421 gaaaaaataataagaatttttgcagagttttgtacatatattgtcccaaatgttccatcaac 480
 QY 481 ACTTCTTGA 489
 Db 481 acttcttga 489

RESULT 2
 AAQ84584

ID

XX

AC

XX

DT

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DE

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KW

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KW

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OS

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AAQ84584 standard; cDNA; 489 BP.

AAQ84584;

04-SEP-1995 (first entry)

Human IL-15 clone 141.hETF.

Interleukin-15; IL-15; hIL-15; T-cell growth factor;

antitumor; virucide; ss.

Homo sapiens.

Location/Qualifiers

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/product= IL-15 precursor

1..144

/*tag= b

145..486

/*tag= c

/product= mature IL-15

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mat_peptide

mat_peptide

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Anderson DM, Eisenman JR, Fung V, Grabstein KH;

Rauch C;

WPI; 1995-082473/11.

P-PSDB; AAR66927.

New purified interleukin-15 - which induces T cell proliferation

and differentiation, used for the treatment of tumours and viral

infection

Disclosure; Page 28-29; 47pp; English.

A sIL-15 probe was prepared from isolated simian interleukin-15

cDNA and used to screen a cDNA library generated from the IMTLH

cell line derived from human bone marrow stromal cells. Clone

141.hETF encoded human IL-15.

Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 16; Length 489;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTCTACTTGTGTTACTT 60

Db 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctacttgtgttactt 60

QY 61 CTAACAGCTCAATTTCTTAACAGCTGGCATTCATGTCCTTCAATTTGGGCTGTTCACT 120

Db 61 cttaacagctcattttcttaactgaagctggcattcattcttcttcttcttcttctt 120

QY 121 GCAGGGCTTCTAAACAGAACGCACTGGTGAATGTAATAGTATTTGAAAAAATT 180

Db 121 gcagggtcttctaaacagaaacagcaactgggtgaatgtaataagtatttgaaaaaatt 180

QY 181 GAAGATCTTATTCATCTATGCTATGCTACTTTATATACGGAAGTGTGTTTCAAC 240

Db 181 gaagatcttattcaatctatgcatattgacttactttatatatacggaaagtgtgttcaac 240

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Db	241	ccccggtgcaagtaacagcaaatgaagtgtcttctcttgagggtacaaagtatttcaactt	300
QY	301	GAGTCGGGAGATCAAGTATTTCATGATACAGTAGAAATCTGATCATCCTAGCAACAACAC	360
Db	301	gagtcgggagatcagagtattcatgatcagtagaaaaatctgatcatcctagcaaacac	360
QY	361	AGTTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAAAGATGTGAGGAATGGAG	420
Db	361	agtttcttctaagtgggaatgtaacagaatctggatgcaagaatgtgaggaactggag	420
QY	421	GAAAAAATATTAAGAAATTTTGGCAGAGTTTGTGATACATATTGTCCAAATGTTTCATCAAC	480
Db	421	gaaaaaataattaagaatttttgcagagttttgtacatatgttgcacaaatgttcatcaac	480
QY	481	ACTTCTTGA 489	
Db	481	actcttga 489	
RESULT 3			
AAT49455			
ID	AAT49455 standard; cDNA; 489 BP.		
XX	AAT49455;		
XX	11-MAR-1997 (first entry)		
DT			
XX	Simian epithelium derived T cell factor cDNA.		
DE			
XX	SETF; African green monkey; CV1/EBNA cell; T-cell; B-cell;		
KW	lymphocyte; proliferation; differentiation; gastrointestinal;		
KW	HIV infection; human immunodeficiency virus; ss.		
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OS	Cercopithecus aethiops.		
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PN	US5574138-A.		
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PD	12-NOV-1996.		
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PF	08-MAR-1993;	93US-0031399.	
XX			
PR	22-FEB-1995.	95US-0393305.	
PR	08-MAR-1993.	93US-0031399.	
PR	22-APR-1994.	94US-0233606.	
XX			
PA	(IMV) IMMUNEX CORP.		
XX			
PI	Anderson DM;	Eisenman JR, Fung V, Grabstein KH;	
PI	Rauch C;		
XX			
DR	WPI; 1996-517923/51.		
DR	P-PSDB; AAW09098 and AAW09099.		
XX			
PT	New epithelium derived T cell factor - induces proliferation of T		
PT	and B cells; stimulates destruction of tumour and virus-infected		
PT	cells and protects against toxicity, partic. for treating intestinal		
PT	disease and HIV infection		
XX			
PS	Claim 1; Fig 1; 35pp; English.		
XX			
CC	The simian ETF (epithelium derived T cell factor) was isolated from		
CC	African green monkey CV1/EBNA cell conditioned medium. The N-		
CC	terminal sequence of the purified SETF was determined and then PCR		
CC	primers were designed based on the sequence information A 92 bp		

CC	fragment was amplified from CVI/EBNA DNA and was used as a probe to screen a CVI/EBNA cDNA library for the full-length SEFF coding sequence (i.e. the present sequence). Mature SEFF induces proliferation and/or differentiation of precursor or mature T cells and is useful for promoting long-term in vitro culture of T-lymphocytes and T-cell lines. It is used for treating gastrointestinal diseases including peptic ulcer, colitis and malignancy and for treating HIV infection.
XX	
SQ	Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;
<hr/>	
	Query Match 100.0%; Score 489; DB 17; Length 489; Best Local Similarity 100.0%; Pred. No. 5.7e-117; Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps
QY	1 ATGAGATTTCGAACACATTTTGAGAAGTATTTCATCCAGTCGTACTTGCTTTACTT 60
DB	1 atgagaatttcgaacacacatttggagaagtatttccatccagtgctacttgtttcactt 60
QY	61 CTAAACAGTCAATTTTAACTGAAGCGGGCATTCATCTCTTCATTTGGSGCTGCTTTCAGT 120
DB	61 ctaaacagtcattttctaactgaagctggcatcacgtcttcattttg9gcgtgccagt 120
QY	121 GCAGGGCTTCCTAAACAGAAGCCAACCTGGGTGAATGTATAAGTAGTTTGAAAAAATT 180
DB	121 gcagggtctcctaaaacagagaagccaactgggtgaatgaataagtatttgaaaaaatt 180
QY	181 GAAGATCTTATTCAATCTATGCATATTGTAGCGTACTTTATATACGGAAGTGATGTTTCA 240
DB	181 gaagatcttattcaatctatgcatattgatgctactttatatatcgaaagtgatgttcac 240
QY	241 CCCAGTTGCCAAAGTAACAGCAATGAAGTGCCTTTCTCTTGGAGTTACAAGTTATTTCAC 300
DB	241 cccagttgccaaagtaacagcaatgaagtcgcttctctcctggagttacaagtctatccact 300
QY	301 GAGTCCGGAGATGCAAGTATTCATGATPACAGTACAGTACAGTAATACTGATCCTAGCAAA 360
DB	301 gagtccggagatgcaagtatttcattcatgatacagtagaatactgatccctagcaaacac 360
QY	361 AGTTTGCTCTTAATGGGAATGTAACAGATCTGGATGCAAAAAGTCTGAGGAACCTGGAG 420
DB	361 agtttgctctctaattgggaatgtaacagaactcggatgcaagaagtgtagggaactggag 420
QY	421 GAAAAAATAATTAAGAAGATTTTTGCACAGTTTTGTACATATTGTCCAAATGTTTCATCAAC 480
DB	421 gaaaaaataattaagaatttttgcagaggttttgcacattttgtccaatgttccaatgttccatcaac 480
QY	481 ACTTCTTGA 489
DB	481 acttcttga 489
<hr/>	
RESULT	4
AAT42243	
ID	AAT42243 standard; DNA; 489 BP.
XX	
AC	AAT42243;
XX	
DT	05-FEB-1997 (first entry)
DE	Human epithelium-derived T cell factor gene.
KW	Epithelium-derived T-cell factor; simian; human; culture; proliferati
KW	epithelial cell; differentiation; T-lymphocyte; African green monkey;
KW	primer; PCR; polymerase chain reaction; amplification; probe; ss.
OS	Homo sapiens.
XX	
FH	key Location/Qualifiers
FT	sig_peptide 1..144
FT	/*tag= a
FT	mat_peptide 145..486

```

FT XX      /*tag= b
XX XX      US5552303-A.
XX XX      03-SEP-1996.
XX XX      08-MAR-1993; 93US-0031399.
XX XX      08-MAR-1993; 93US-0031399.
XX XX      (IMMV ) IMMUNEX CORP.
XX XX      Anderson D, Eisenman J, Fung V, Grabstein K, Rauch C;
XX XX      WPI; 1996-412063/41.
XX XX      P-PSDB; AA07255.
XX XX      New isolated simian and human epithelium-derived T-cell factors -
XX XX      which stimulate the proliferation and/or differentiation of
XX XX      T-lymphocytes and T-cell lines
XX XX      Claim 21: Column 23-24; 22pp; English.
XX XX      This is the nucleotide sequence encoding a human epithelium-derived
XX XX      T-cell factor (ETF). The gene was obtained using a 1.37 kb fragment of
XX XX      the corresp. African green monkey gene (AA742242) as a probe to screen a
XX XX      cDNA library constructed from RNA derived from the IMTLH cell line.
XX XX      This cell line is derived by stable transformation of a human bone
XX XX      marrow stromal cell culture with pSV3neo. From a pool of about 1000 cDNA
XX XX      clones, one clone I41.hETF contained this sequence. ETF is a protein of
XX XX      15-17 kD which is expressed by epithelial cells and stimulates
XX XX      proliferation and/or differentiation of precursor and/or mature T cells.
XX XX      The protein is therefore useful for promoting long term in vivo culture
XX XX      of T-lymphocytes and T-cell lines.
XX XX      Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match      100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACACATTTGAGAGTATTTCCATCCAGTGGTACTGTGTTTACTTT 60
DB 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctactgtgtttacttt 60
QY 61 CTAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
DB 61 ctaaacagctcatTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
QY 121 GCAGGGCTTCCTAAACAGAGCCCACTGGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 gcagggttcctaaacagagcccaactgggtgaatgtaataagtattgaaaaaattt 180
QY 181 GAAGATCTTATTCATCTATGCATATTCATCTACTTTATATACGGAAGTGTTCAC 240
DB 181 gaagatcttatttcattctatgcataatctactttatatacggaaagtgtttcac 240
QY 241 CCCAGTTGCCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAGTATTTTCACTT 300
DB 241 cccagttgccaaagtaacagcaatgaagtgtcttcttggagttacagatttttcactt 300
QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTAAATCTGATCATCTCTAGCAACAAC 360
DB 301 gagtcggagatgcaagtatttcattgatacagtagaataatctgatcctcagcaacaac 360
QY 361 AGTTTGCTTCTAATGGAATGTAACAGATCTGGATGCAAGAAATGTGAGGAAGTGGAG 420
DB 361 agtttgcttcttaatgggaattgtaacagatctggatgcaagaagtgtgaggaactggag 420
QY 421 GAAAAAATATTAAAGAAATTTTTCACAGTGTTCATACATATTTGCCAAATGTTTCATCAAC 480
DB 421 gaaaaaataattaaagaatttttgcagagttttgcacatatttgcacaaatgttccatcaac 480

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QY 481 ACTTCTTGA 489
DB 481 acttcttga 489

RESULT 5
AAT36635
ID AAT36635 standard; cDNA; 489 BP.
XX
AC AAT36635;
XX
DT 17-NOV-1996 (first entry)
XX
DE Human interleukin-15 cDNA.
XX
KW Interleukin-15; antagonist; mutein; graft versus host disease;
KW allograft; T-cell growth factor; ss.
XX
OS Homo sapiens.
XX
PN WO9626274-A1.
XX
PD 29-AUG-1996.
XX
PF 21-FEB-1996; 96WO-US02520.
XX
PR 22-FEB-1995; 95US-0392317.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Grabstein KH, Paxton RJ, Pettit DK;
XX
DR WPI; 1996-402367/40.
DR P-PSDB; AAR98527.
XX
PT Antagonists of interleukin-15 - are used to treat patients having
PT symptoms of graft-versus-host disease and for prolonging allo:graft
PT survival
XX
PS Disclosure; Page 25; 32pp; English.
XX
CC A cDNA clone (AAT36635) codes for human interleukin-15 (IL-15)
CC (AAR98527), a T-cell growth factor. Muteins of human IL-15 or
CC simian IL-15 (see also AAR98526) are useful as antagonists of IL-15
CC and can be prep. by PCR-mediated mutagenesis of the encoding
CC sequences. Preferred muteins have amino acid substitutions at
CC Asp56 and/or Gln156 of the IL-15 protein that prevent signal
CC transduction. They are useful for treating graft-versus-host
CC disease and for prolonging allograft survival.
XX
SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

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Query Match      100.0%; Score 489; DB 17; Length 489;
Best Local Similarity 100.0%; Pred. No. 5.7e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACACATTTGAGAGTATTTCCATCCAGTGGTACTGTGTTTACTTT 60
DB 1 atgagaatttcgaacacacatttgagaagtatttccatccagtgctactgtgtttacttt 60
QY 61 CTAACAGCTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
DB 61 ctaaacagctcatTTTCTAACTGAAGCTGGCATTCATGCTTCATTTTGGGCTGTTTCACT 120
QY 121 GCAGGGCTTCCTAAACAGAGCCCACTGGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 gcagggttcctaaacagagcccaactgggtgaatgtaataagtattgaaaaaattt 180
QY 181 GAAGATCTTATTCATCTATGCATATTCATCTACTTTATATACGGAAGTGTTCAC 240
DB 181 gaagatcttatttcattctatgcataatctactttatatacggaaagtgtttcac 240

```

QY 241 CCAGTTCGAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTTCACTT 300
|||||
Db 241 ccagttgcaagtaacagcaatgaagtgtcttctcttggtgagttacaagttatttcactt 300

QY 301 GAGTCGGGAGTCAAGTATTTCATGATACAGTAGAATAATCTGATCATCTTACGCAACAAC 360
|||||
Db 301 gagtcgggagtcagagttatttcattgacagtagaataatctgacatctctagcaacaac 360

QY 361 AGTTGCTCTCTTAATGGGAATCTAACAGAACTCTGGAATGCAAGAAATGTGAGGAACCTGGAG 420
|||||
Db 361 agttgtctctctaaatgggaatgaacagaatctggatgcaagaatgtgaggaactggag 420

QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGCTTTTGACATATTGTCGCAAAATGTTTCATCAAC 480
|||||
Db 421 gaaaaaatattaaagaattttgcagagttttgtacatatgtgtccaaatgtttcatcaac 480

QY 481 ACTTCTTTGA 489
|||||
Db 481 actctcttga 489

RESULT 6
AAT58404
ID AAT58404 standard; cDNA; 489 BP.
XX
AC AAT58404;
XX
DT 18-MAR-1997 (first entry)
XX
DE Interleukin-15 coding sequence.
XX
KW IL-15; interleukin-15; T-cell growth factor; proliferation; stimulate;
KW muscle growth; differentiation; hypertrophy; treat; atrophy; wasting;
KW skeletal; cardiac; muscle; congestive heart failure; diabetes-associated;
KW glucose-intolerance; dyslipidaemia; rhabdomyosarcoma; dystrophy; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..489
FT FT /*tag= a
FT ET /product= IL-15
XX
PN WO9637223-Al.
XX
PD 28-NOV-1996
XX
PF 07-MAY-1996; 96WO-US06423.
XX
PR 24-MAY-1995; 95US-0535733.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Grabstein KE, Quinn LS, Troutt AB;
XX
DR WPI; 1997-020939/02.
DR P-PSDB; AAW01658.
XX
PT Muscle trophic compsn. contg. interleukin 15 - for treating, e.g.
PT congestive heart failure, muscle wasting etc.
XX
PS Disclosure; Page 12; 22pp; English.
XX
CC This sequence encodes human interleukin-15 (IL-15) (see AAW01658), a
CC known T-cell growth factor that can support proliferation of an
CC IL-2-dependent cell line, C2LL-2. Compsns. contg. IL-15 to stimulate
CC muscle growth, differentiation or hypertrophy are claimed. The
CC stimulation of muscle growth is useful for treating atrophy, or wasting,
CC in particular, skeletal and cardiac muscle atrophy. The compsn. further
CC comprises a steroid, growth hormone and insulin-like growth factor.
CC Congestive heart failure, muscle wasting and diabetes-associated
CC glucose-intolerance or dyslipidaemia, rhabdomyosarcoma and muscular

CC dystrophy can all be treated by such compsns..

SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 18; Length 489;

Best Local Similarity 100.0%; Pred. No. 5.7e-117;

Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCATCCAGTCTACTTGTCTTACTT 60
|||||

Db 1 atgagaatttcgaaacacacatttgagaagtatttcacatccagtgactgttactt 60
|||||

QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTCTTCAATTTTGGGCTGTTTCAGT 120
|||||

Db 61 ctaaacagtcattttctaaactgaagctggcattcatgtcttcatttttggctgtttcagt 120
|||||

QY 121 GCAGGGCTTCCTAAACAGACGACCAACTGGTGCAATGTAATGAATGTTGAAAAAATTT 180
|||||

Db 121 gcagggcttcctaaacagacagacccaactgggtgaatgaatgatttgaaaaaatt 180
|||||

QY 181 GAAGATCTTATTCATCTATGATATTGATGCTACTTTATATACGGAAGTGTGTTTCCAC 240
|||||

Db 181 gaagatcttattcaatctatgcatattgatgctactttatatatacggaaagtgtttcac 240
|||||

QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTTATTTTCACTT 300
|||||

Db 241 cccagttgcaagtaacagcaatgaagtgtcttctctgttgagttacaagtatttcactt 300
|||||

QY 301 GAGTCGGGAGTCAAGTATTTCATGATACAGTAGAATAATCTGATCATCTTACGCAACAAC 360
|||||

Db 301 gagtcgggagtcagagttatttcattgacagtagaataatctgacatctctagcaacaac 360
|||||

QY 361 AGTTGCTCTCTTAATGGGAATGTAACAGAACTCTGGATGCAAGAAATGTGAGGAACCTGGAG 420
|||||

Db 361 agttgtctctctaaatgggaatgaacagaatctggatgcaagaatgtgaggaactggag 420
|||||

QY 421 GAAAAAATATTAAAGAAATTTTGCAGAGTTTGTGACATATTGTCGCAAAATGTTTCATCAAC 480
|||||

Db 421 gaaaaaatattaaagaattttgcagagttttgtacatatgtgtccaaatgtttcatcaac 480
|||||

QY 481 ACTTCTTTGA 489
|||||

Db 481 actctcttga 489
|||||

RESULT 7

AAV23554

ID AAV23554 standard; cDNA; 489 BP.

XX

AC AAV23554;

XX

DT 13-JUL-1998 (first entry)

XX

DE Human interleukin-15 coding sequence.

XX

KW Human; interleukin-15; IL-15; T cell; B cell; proliferation; vaccine;

KW cytokine; growth factor; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 1..489

FT FT /*tag= a

XX

PN US5747024-A.

XX

PD 05-MAY-1998.

XX

PF 19-JUN-1995; 95US-0504042.

XX

PR 19-JUL-1995; 95US-0504042.

PR 08-MAR-1993; 93US-0031399.

XX Homo sapiens.
 XX WO200002582-A2.
 XX PD 20-JAN-2000.
 XX PF 09-JUL-1999; 99WO-GB02201.
 XX PR 10-JUL-1998; 98GB-0014892.
 XX PA (KENN-) KENNEDY INST RHEUMATOLOGY MATHILDA & TER.
 XX PI Londel M, Quaratino S, Maiuri L;
 XX WPI; 2000-171080/15.
 XX DR P-PSDB; AAY78595.
 XX Use of antagonists of interleukin-15 for treating an inflammatory bowel
 XX disease, particularly celiac disease -
 XX PS Disclosure; Page 70; 70pp; English.
 XX This sequence represents the human interleukin 15 (IL-15) nucleotide
 XX sequence. The IL-15 nucleotide sequence and the protein encoded by it can
 XX be used to determine and create antagonists of IL-15. An antagonist of
 XX IL-15 can be used for treating an inflammatory bowel disease (IBD). The
 XX invention relates to the treatment of celiac disease using IL-15
 XX antagonists. The antagonists are preferably muteins of IL-15, antibodies
 XX against IL-15 or IL-15 molecules bound to chemical groups that interfere
 XX with the ability of IL-15 to effect a signal transduction through either
 XX the alpha or the gamma subunit of the IL-15 receptor complex. The IL-15
 XX antagonists of the invention can be used to treat irritable bow disease
 XX especially celiac disease.
 XX SQ Sequence 489 BP; 159 A; 79 C; 95 G; 156 T; 0 other;

Query Match 100.0%; Score 489; DB 21; Length 489;
 Best Local Similarity 100.0%; Pred. No. 5.7e-117;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGAGATTTTCGAAACCAATTTGAGAGTATTTCCATCCAGTCTACTTGTGTTACTT 60
 DB 1 atgagatttcgaaaccacattgagagattttccatccagtgctacttgtgttactt 60
 QY 61 CTAACAGTCAATTTTCTAAGTGAAGTGGCATTCATGCTCTTCATTTGGGCTGTTTCACT 120
 DB 61 cttaacagtcattttcttaagtgagctggcatttcatttcttcattttgggtgttcaagt 120
 QY 121 GCAGGGCTTCTAAACAGAGCCCACTGGGTGAATGTAATGTAATGTAATGTAATGTAAT 180
 DB 121 gcagggtcttctaaacagagcccaactgggtgaatgtaataagtgatttgaaaaaatt 180
 QY 181 GAAGATCTTATTCATCTATCATATTCATCTACTTATATACGGAAGTGAATGTAAT 240
 DB 181 gaagatcttattcatctatcatattgatctacttattatatacggaagtgaatgtaatt 240
 QY 241 CCCAGTTCGAAGTAACAGCAATGAAGTGTCTTCTTGGAGTACAGTATTTTCACTT 300
 DB 241 cccagttcgaaagtaacagcaatgaagtgcttctcttgaggtacagatttttcaactt 300
 QY 301 GAGTCCGAGATGCAAGTATTCATGATACAGTAGAATACTGATCATCTAGCAAAACAC 360
 DB 301 gagtccgagatgcaagtattcatgatacatagataagataatctgatcctctagcaaacac 360
 QY 361 AGTTGTCTTCTAATGGAAGTAAACAGCAATCTGGATCAAGATGCAAGTCACTGGAG 420
 DB 361 agttgtcttcttaatgggaagttaaacagcaatctggatcaagatgcaagtaactggag 420
 QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGAGTTTGTACATATTTGCCAAATTTTCATCAAC 480
 DB 421 gaaaaaataataagaatttttcagagagtttgtacatatttgcctcaattgtcccaatttcatcaac 480

QY 481 ACTTCTTGA 489
 DB 481 acttcttga 489
 RESULT 11
 AAZ38244
 ID AAZ38244 standard; cDNA; 489 BP.
 XX AC AAZ38244;
 XX DT 09-FEB-2000 (first entry)
 XX DE Simian epithelium-derived T-cell factor (ETF) cDNA.
 KW ETF; epithelium-derived T-cell factor; T-cell; T-lymphocyte;
 KW proliferation; differentiation; growth factor; precursor; mature; CD4+;
 KW CD8+; gastrointestinal; epithelium; cell culture; treatment; HIV;
 KW gastrointestinal disease; gastroenteritis; colitis;
 KW inflammatory bowel disease; villus atrophic disorder; enteritis;
 KW chemotherapy; radiotherapy; gut toxicity; cancer; side effect;
 KW tolerated dose; ss.
 XX OS Mammalia.
 XX FH Key Location/Qualifiers
 XX CDS 1..489 /*tag= a
 XX FT /product= "Simian ETF precursor protein (AAZ52308)"
 XX FT 1..144 /*tag= b
 XX FT sig_peptide 145..489
 XX FT mat_peptide /*tag= c
 XX FT /product= "Mature simian ETF (AAZ52309)"
 XX PN US5985262-A.
 XX PD 16-NOV-1999.
 XX PF 03-FEB-1997; 97US-0794524.
 XX PR 22-FEB-1995; 95US-0393305.
 XX PR 04-OCT-1996; 96US-0726817.
 XX PR 08-MAR-1993; 93US-0031399.
 XX PR 22-APR-1994; 94US-0233606.
 XX PA (IMMV) IMMUNEX CORP.
 XX PI Rauch C, Fung V, Eisenman JR, Grabstein KH, Anderson DM;
 XX WPI; 2000-022267/02.
 XX DR P-PSDB; AAY52308, AAY52309.
 XX ST Stimulation of T-cells in human immunodeficiency virus infected
 XX patients -
 XX PS Claim 1; Columns 35-36; 33pp; English.
 CC This sequence represents simian epithelium-derived T-cell factor (ETF)
 CC cDNA. ETF is a previously unidentified T-cell growth factor which
 CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate
 CC and differentiate. It also promotes proliferation of the gastrointestinal
 CC epithelium. The protein can be used to promote long-term in vitro culture
 CC of T-lymphocytes and T-cell lines. ETF can be used for treating HIV
 CC infection, HIV-associated diseases, and other diseases or conditions
 CC where stimulation of T-cell proliferation would be desirable e.g., it
 CC could be used to augment the destruction of tumour cells or virally-
 CC infected cells. ETF may also be used to treat or prevent gastrointestinal
 CC disease, including chemotherapy and radiotherapy associated enteritis,
 CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic
 CC disorders. Chemotherapy and radiotherapy associated enteritis (gut
 CC toxicity) results in bleeding and sepsis due to gastrointestinal flora


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XX 29-OCT-1998; 98WO-IB01837.
XX 31-OCT-1997; 97US-0962503.
XX (HISM ) HISAMITSU PHARM CO LTD.
XX Hamanaka S, Nozawa I, Veerapaneni D;
XX WPI; 1999-313334/26.
XX New ribozymes targeted to interleukin-15 mRNA
XX Disclosure; Fig 8; 46pp; English.
XX The present sequence describes an isolated RNA molecule which
XX specifically cleaves mRNA encoding interleukin 15 (IL-15). The
XX enzymatic RNA molecules can bind to and cleave mRNA encoding IL-15.
XX They can be used for treating disorders associated with IL-15 such
XX as inflammatory disorders, e.g. rheumatoid arthritis by inhibiting
XX the synthesis of IL-15 in lymphocytes and preventing the recruitment
XX and activation of macrophages. They can also be used to develop
XX transgenic animals which can be used to identify the impact of
XX increased or decreased IL-15 levels on a particular pathway or
XX phenotype. The present sequence represents a human IL-15 DNA sequence.
XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

Query Match 100.0%; Score 489; DB 20; Length 1202;
Best Local Similarity 100.0%; Pred. No. 7.2e-117; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

QY 1 ATGAGATTTCGAACACACATTGAGAGTATTTCATCCAGTCGCTACTTGTGTACTT 60
DB 317 atgagatttcgaacacacattgagagattttccatccagtcgctactgtgtactt 376
QY 61 CTAAACAGTCATTTCTACTGAAGTCGGATTCATGCTCTTCAATTTGGCTGTTTCAGT 120
DB 377 ctaaacagtcattttctactgaagtcggatcattcattctcttctgttgcagt 436
QY 121 GCAGGGCTTCCTAAACAGAGCCAACTGGTGAATGTAATAGTCATTGAAAAAATT 180
DB 437 gcagggttcctaaacagagccaaactgggtgaatgtaatagtcatttgaataaatt 496
QY 181 GAAGATCTTATTCATCTATGCAATATGATGCTACTTTATATACGGAAGTATGTCAC 240
DB 497 gaagatcttattcaatctatgcatattgctactttatatacggaaagtgtgtcac 556
QY 241 CCCAGTTGCAAGTACACGAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACTT 300
DB 557 cccagttgcaagtacacgaatgaagtccttctcttggagttacaagttatttcactt 616
QY 301 GAGTCCGGAGATGCAAGTATTTCATGATACAGTAGAAAACTGTATCTAGCAACAAC 360
DB 617 gagtccggagatgcaagatttcattgatatacagtagaataatctgatcatctagcaacaac 676
QY 361 AGTTCTCTCTTAATGGGAATGTAACAGATCTGGATGCAAGAATGTGAGGAACGGAG 420
DB 677 agttctctcttaatgggaatgtaacagaatctggatgcaagaatgtgaggaactggag 736
QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTGACATATTTGTCGAATGTTTCATCAAC 480
DB 737 gaaaaaataattaaagaatttttcagagtttgtgacattttgtacatttgcataattgttccaaatgttccatcaac 796
QY 481 ACTTCTTGA 489
DB 797 acttctctga 805

RESULT 15
AAF21342
ID AAF21342 standard; DNA; 1202 BP.
```

XX AAF21342;
XX 14-MAR-2001 (first entry)
XX Human low adenosine antisense oligonucleotide related sequence #2909.
XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
XX human; airway disorder; bronchoconstriction; lung inflammation;
XX surfactant depletion; respiratory; bronchodilator; antiinflammatory;
XX immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
XX respiratory obstruction; pulmonary obstruction; impeded respiration;
XX surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
XX respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
XX pulmonary hypertension; emphysema; pulmonary transplantation rejection;
XX chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
XX cancer; ss.
XX Homo sapiens.
XX OS
XX WO200062736-A2.
XX 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US08020.
XX 06-APR-1999; 99US-0127958.
XX (UYEC-) UNIV EAST CAROLINA.
XX (NYCE/) NYCE J W.
XX Nyce JW;
XX WPI; 2000-679539/66.
XX Low adenosine (A) content antisense oligonucleotides which do not
XX trigger adenosine receptors during metabolism, useful e.g. for treating
XX cancers and respiratory obstructions -
XX Disclosure; Page 1344-1345; 1592pp; English.
XX The present invention describes low adenosine (A) content antisense
XX oligonucleotides and compositions (I) comprising them. In the antisense
XX oligonucleotides the A is replaced by a 'Universal' or alternative base.
XX (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
XX immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
XX The antisense oligonucleotides and (I) can be used to down-regulate the
XX expression and or activity of target polypeptides associated with
XX lung/respiratory disorders and malignancies, such as stimulating and
XX activating peptide factors and transmitters, transcription factors,
XX immunoglobulins and antibodies, antibody receptors, cytokines and
XX chemokines, endogenously produced specific and non-specific enzymes,
XX binding proteins, adhesion molecules and their receptors, cytokine and
XX chemokine receptors, adenosine receptors, bradykinin receptors, central
XX nervous system (CNS) and peripheral nervous and non-nervous system
XX transmitters, defensins, growth factors, vasoactive peptides and
XX receptors, binding proteins and malignancy associated proteins. The
XX antisense oligonucleotides may be used in this way to treat disorders
XX including respiratory obstruction (especially pulmonary obstruction
XX and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
XX and/or surfactant hypoproduction which are associated with a disease or
XX condition selected from pulmonary vasoconstriction, inflammation,
XX allergies, asthma, impeded respiration, respiratory distress syndrome
XX (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
XX pulmonary transplantation rejection, pulmonary infections, bronchitis,
XX and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
XX fragments and antisense oligonucleotides used in the exemplification of
XX the present invention.
XX Sequence 1202 BP; 355 A; 219 C; 249 G; 379 T; 0 other;

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Query Match      100.0%; Score 489; DB 21; Length 1202;
Best Local Similarity 100.0%; Pred. No. 7.2e-117;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 317 atgagaatttcgaaccacatttgagaagtatttccatccagtgctacttggtttactt 376

QY 61 CTAACAGTCATTCTTAACCTGAAGCTGGCATTTCATGCTCTTTCATTTGGGCTGTTTCAGT 120
Db 377 ctaaacagtcattcttaactgaagctggcattcattgtcttcttcttgggctgtttcagt 436

QY 121 GCAGGGCTTCCTAAACAGAACGCCAAGTGGTGAATGTAATTAAGTGAATTTGAAAAAATT 180
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QY 181 GAAGATCTTATTCATCTATGATATTTGATGCTACTTATATATACGGAAGTGTTCAC 240
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QY 241 CCCAGTTGCAAAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTACAAGTTATTTTCACTT 300
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QY 301 GAGTCGGGAGATGCAAGTATTCATGATACAGTAGAAGAAATCTGATCATCTCTAGCAAAACAAC 360
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QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTGACATATTGTCCAAATGTTTCATCAAC 480
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QY 481 ACTTCTTGA 489
Db 797 acttcttga 805

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Search completed: September 19, 2002, 23:25:03
Job time: 4503 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:33:45 ; Search time 43.55 Seconds
(without alignments)
2758.089 Million cell updates/sec

Title: US-09-196-427-2
Perfect score: 489
Sequence: 1 ATGAGATTTCGAACACCA.....TGTTCAACACACTTCTTGA 489

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	489	100.0	489	1	US-08-031-399-4
2	489	100.0	489	1	US-08-393-305-1
3	489	100.0	489	1	US-08-535-733-1
4	489	100.0	489	1	US-08-726-817-1
5	489	100.0	489	1	US-08-504-042-4
6	489	100.0	489	1	US-08-392-317B-2
7	489	100.0	489	2	US-08-725-969-1
8	489	100.0	489	2	US-08-794-524-1
9	489	100.0	489	3	US-09-134-132-2
10	489	100.0	489	4	US-09-134-134A-2
11	489	100.0	489	4	US-09-134-456-2
12	489	100.0	489	4	US-09-196-427-2
13	489	100.0	489	4	US-09-189-193-1
14	489	100.0	489	5	PCT-US94-03793-4
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16	489	100.0	1202	3	US-08-962-503-11
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19	465	95.1	489	1	US-08-031-399-1
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21	465	95.1	489	1	US-08-726-817-4
22	465	95.1	489	1	US-08-504-042-1
23	465	95.1	489	1	US-08-392-317B-1
24	465	95.1	489	2	US-08-725-969-4
25	465	95.1	489	2	US-08-794-524-4
26	465	95.1	489	3	US-09-134-132-1
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29 465 95.1 489 4 US-09-196-427-1 Sequence 1, Appli
30 465 95.1 489 4 US-09-189-193-4 Sequence 4, Appli
31 465 95.1 489 5 PCT-US94-03793-1 Sequence 1, Appli
32 378.4 77.4 1248 4 1248 1 US-09-200-141-1 Sequence 1, Appli
33 345 70.6 345 1 US-08-393-305-12 Sequence 12, Appli
34 345 70.6 345 1 US-08-726-817-12 Sequence 12, Appli
35 345 70.6 345 2 US-08-725-969-12 Sequence 12, Appli
36 345 70.6 345 2 US-08-794-524-12 Sequence 12, Appli
37 345 70.6 345 4 US-09-189-193-12 Sequence 12, Appli
38 325.8 66.6 345 1 US-08-393-305-13 Sequence 13, Appli
39 325.8 66.6 345 1 US-08-726-817-13 Sequence 13, Appli
40 325.8 66.6 345 2 US-08-725-969-13 Sequence 13, Appli
41 325.8 66.6 345 2 US-08-794-524-13 Sequence 13, Appli
42 325.8 66.6 345 4 US-09-189-193-13 Sequence 3, Appli
C 43 45.6 9.3 60 3 US-08-842-947-3 Sequence 11, Appli
44 37.8 7.7 37948 4 US-09-251-645-11 Sequence 42, Appli
45 36.6 7.5 3660 1 US-08-158-232-42

ALIGNMENTS

RESULT 1
US-08-031-399-4
; Sequence 4, Application US/08031399
; Patent No. 5552303
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: Epithelium-derived T-cell Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/031,399
; FILING DATE: 19930308
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: 2811
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-031-399-4

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

SOFTWARE PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2833
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-535-733-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

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DB 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTGCTGTTTACTT 60
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCAATTCATGCTGCTGTTTGGGCTGTTTCACT 120
DB 61 CTAACAGTCATTTTCTAACTGAAGTGGCAATTCATGCTGCTGTTTGGGCTGTTTCACT 120
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DB 121 GCAGGCTTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
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DB 181 GAAGATCTTATTCATCTATGATATGATAGTAAAGTCTGATCATCTAGCAACAAC 240
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QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCAAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTGACATATTTGCAAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 4
US-08-726-817-1
Sequence 1, Application US/08726817
Patent No. 5707616
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June

APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIAL-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-726-817-1

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

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DB 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTGCTGTTTACTT 60
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DB 61 CTAACAGTCATTTTCTAACTGAAGTGGCAATTCATGCTGCTGTTTGGGCTGTTTCACT 120
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DB 121 GCAGGCTTCCCTAAACAGAGCCAACTGGTGAATGTAATAGTCAATTTGAAAAAATT 180
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DB 421 GAAAAAATATTAAGAATTTTTCAGAGTTTGTACATATTTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 5
US-08-504-042-4
; Sequence 4, Application US/08504042
; Patent No. 5747024
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: Epithelium-derived T-cell Factor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/504,042
; FILING DATE: 19-JUL-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,399
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Launer, Charlene
; REGISTRATION NUMBER: 33,035
; REFERENCE/DOCKET NUMBER: 2811
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-504-042-4

Query Match 100.0%; Score 489; DB 1; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 6
US-08-392-317B-2
; Sequence 2, Application US/08392317B
; Patent No. 5795966
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,317B
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-08-392-317B-2

Query Match 100.0%; Score 489; DB 1; Length 489;

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Best Local Similarity 100.0%; Pred. No. 1.6e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 489; Conservative 0;

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Db 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
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Db 121 GCAGGGCTTCTTAAACAGAACCAACTGGTGAATGTAATAGTCAATTTGAAAAAAT 180
QY 181 GAAGATCTTATCAATCTATGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 240
Db 181 GAAGATCTTATCAATCTATGATGCTACTTTATATACGGAAGTGAATGTTTCAAC 240
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Db 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAGTCTGATCATCTAGCAAAAC 360
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QY 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTTCGAGAGTTTGTACATATTTGCCAAATGTTTCAATCAAC 480
Db 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTTCGAGAGTTTGTACATATTTGCCAAATGTTTCAATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 7
US-08-725-969-1
; Sequence 1, Application US/08725969
; Patent No. 5892001
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,969
; FILING DATE: 04-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/393,305
; FILING DATE: 22-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Mcmasters, David D.
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; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 480052.409C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-622-4900
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
; US-08-725-969-1

Query Match 100.0%; Score 489; DB 2: Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124; Mismatches 0; Indels 0; Gaps 0;
Matches 489; Conservative 0;

QY 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
Db 1 ATGAGAAATTCGAAACACACATTTGAGAAGTATTTCCATCCAGTGCCTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTCTTAAGTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTCTTAAGTGAAGCTGGCAATTCATGCTCTTCAATTTGGGCTGTTTCAGT 120
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAAGTCTGATCATCTAGCAAAAC 360
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Db 421 GAAAAAATATTAAGAAATTTTTCAGAGTTTTCGAGAGTTTGTACATATTTGCCAAATGTTTCAATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 8
US-08-794-524-1
; Sequence 1, Application US/08794524
; Patent No. 5985262
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June
; APPLICANT: Fung, Victor
; APPLICANT: Rauch, Charles
; TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed and Berry
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
```

STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/794,524
FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-08-794-524-1

Query Match 100.0%; Score 489; DB 2; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTTACTT 60
DB 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 120
QY 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180
DB 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180
QY 181 GAAGATCTTATTCATCTATGCAATATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 240
DB 181 GAAGATCTTATTCATCTATGCAATATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 240
QY 241 CCAGCTTCAAAAGTAACAGCAATGAAGTCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 300
DB 241 CCAGCTTCAAAAGTAACAGCAATGAAGTCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 300
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DB 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTATGAGTATGATCATCTCTAGCAACCAAC 360
QY 361 AGTTTGTCTTCTTAATGGGAATGTAACAGCAATCTGGATCCAAAGATGTGAGCAACTGGAG 420
DB 361 AGTTTGTCTTCTTAATGGGAATGTAACAGCAATCTGGATCCAAAGATGTGAGCAACTGGAG 420
QY 421 GAAAAAATATTAAGAATATTTTGCAGAGTTTGTGACATATTTGTCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAATATTTTGCAGAGTTTGTGACATATTTGTCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
DB 481 ACTTCTTGA 489

RESULT 9
US-09-134-132-2
Sequence 2, Application US/09134132
Patent No. 6013480
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Paxton, Raymond
APPLICANT: Pettit, Dean
TITLE OF INVENTION: Antagonists of IL-15
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Word for Windows 95, 7.0
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/134,132
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: US/08/392,317
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Malaska, Stephen L.
REGISTRATION NUMBER: 32,655
REFERENCE/DOCKET NUMBER: 2831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-09-134-132-2

Query Match 100.0%; Score 489; DB 3; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTTACTT 60
DB 1 ATGAGAAATTCGAAACCCACATTTGAGAGATATTTCCATCCAGTGTACTTGTGTTTACTT 60
QY 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 120
DB 61 CTAACAGTCATTTCTAACTGAAGCTGGCATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 120
QY 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180
DB 121 GCAGGGCTTCCCTAAACAGAGCCCAACTGGGTGAATGTAATAAGTGATTTGAAAAAATTT 180
QY 181 GAAGATCTTATTCATCTATGCAATATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 240
DB 181 GAAGATCTTATTCATCTATGCAATATTCATGCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 300
DB 241 CCCAGTTGCAAGTAACAGCAATGAAGTCTTCTTCTTGGAGTTTACAAGTTATTTTCACTT 300

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QY 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
Db 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
QY 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATCTGAGGAACCTGGAG 420
Db 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
QY 421 GAAAAAATAATTAAGAAATTTTGGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATAATTAAGAAATTTTGGCAGAGTTTGTACATATTTGTCACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 10
US-09-134-134A-2
; Sequence 2, Application US/09134134A
; Patent No. 6185466
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,134A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-134A-2

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred No. 1.6e-124; Indels 0; Gaps 0;
Matches 489; Conservative 0; Mismatches 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAAGTATTTCCATCCAGTGCCTACTGTGTTACTT 60
Db 1 ATGAGAAATTCGAAACACATTTGAGAAAGTATTTCCATCCAGTGCCTACTGTGTTACTT 60
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QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGTCCTTTCATTTTGGGCTGTTTCAGT 120
Db 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGTCCTTTCATTTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCTCTAAACAGAGCCAACTGGTGAATGTAATGAAGTGAATTTGAAAAAAATTT 180
Db 121 GCAGGGCTTCTCTAAACAGAGCCAACTGGTGAATGTAATGAAGTGAATTTGAAAAAAATTT 180
QY 181 GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAGCTGATGTTTCA 240
Db 181 GAAGATCTTATTCATCTATGTCATATTTGATGCTACTTTATATACGGAAGCTGATGTTTCA 240
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTCTTGGAGTTACAAATTTTTCACCT 300
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QY 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
Db 301 GAGTCGGGAGATCAAGTATTCATGATACAGTAGAGAAATCTGATCATCCTAGCAACAAC 360
QY 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
Db 361 AGTTTCTCTTCTTAATGGGAATGTAAACAGATCTGGATGCAAAAGAAATGTGAGGAACCTGGAG 420
QY 421 GAAAAAATAATTAAGAAATTTTGGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
Db 421 GAAAAAATAATTAAGAAATTTTGGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTGA 489
Db 481 ACTTCTTGA 489

RESULT 11
US-09-134-456-2
; Sequence 2, Application US/09134456
; Patent No. 6186783
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELEPHONE: 206-587-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-134-456-2

Query Match      100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
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DB 1 ATGAGAAATTCGAACACCAATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
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QY 61 CTAACAGTCATTTCTTAACCTGCACTGCAATTCATGCTTCTTCAATTTGGGCTGTTTCACT 120
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DB 61 CTAACAGTCATTTCTTAACCTGCACTGCAATTCATGCTTCTTCAATTTGGGCTGTTTCACT 120
    |||||||

QY 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
    |||||||
DB 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
    |||||||

QY 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTGGGCTGTTTCACT 240
    |||||||
DB 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTGGGCTGTTTCACT 240
    |||||||

QY 241 CCAGCTTGCAGAGTGAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 300
    |||||||
DB 241 CCAGCTTGCAGAGTGAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360
    |||||||
DB 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360
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QY 361 AGTTTGTCTTCTTAATGGAATGTACAGAACTGATCAAGAAATGTGAGGAACTGGAG 420
    |||||||
DB 361 AGTTTGTCTTCTTAATGGAATGTACAGAACTGATCAAGAAATGTGAGGAACTGGAG 420
    |||||||

QY 421 GAAAAAATATTAAGAATTTTTCAGAGAGTTTGTGATACATATTTGTCCAAATGTTTCAATCA 480
    |||||||
DB 421 GAAAAAATATTAAGAATTTTTCAGAGAGTTTGTGATACATATTTGTCCAAATGTTTCAATCA 480
    |||||||

QY 481 ACTTCTTGA 489
    |||||||
DB 481 ACTTCTTGA 489
    |||||||

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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/392,317
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Malaska, Stephen L.
; REGISTRATION NUMBER: 32,655
; REFERENCE/DOCKET NUMBER: 2831
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-597-0430
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 489 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..489
US-09-196-427-2

Query Match      100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAACACCAATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
    |||||||
DB 1 ATGAGAAATTCGAACACCAATTTGAGAGATATTTCCATCCAGTGTCTACTTGTGTTTACTT 60
    |||||||

QY 61 CTAACAGTCATTTCTTAACCTGCACTGCAATTCATGCTTCTTCAATTTGGGCTGTTTCACT 120
    |||||||
DB 61 CTAACAGTCATTTCTTAACCTGCACTGCAATTCATGCTTCTTCAATTTGGGCTGTTTCACT 120
    |||||||

QY 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
    |||||||
DB 121 GCAGGGCTTCCATAACAGAGCCCAACTGGGTGAATGAATGAATGAATGAATGAATGAAT 180
    |||||||

QY 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTGGGCTGTTTCACT 240
    |||||||
DB 181 GAAGATCTTATTCATCTATGCATATTCATGCTTCTTCAATTTGGGCTGTTTCACT 240
    |||||||

QY 241 CCAGCTTGCAGAGTGAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 300
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DB 241 CCAGCTTGCAGAGTGAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 300
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QY 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360
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DB 301 GAGTCCGGAGATGCAAGTATTCATGATACAGTAGAGAAATCTGATCATCTAGCAAAAC 360
    |||||||

QY 361 AGTTTGTCTTCTTAATGGAATGTACAGAACTGATCAAGAAATGTGAGGAACTGGAG 420
    |||||||
DB 361 AGTTTGTCTTCTTAATGGAATGTACAGAACTGATCAAGAAATGTGAGGAACTGGAG 420
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QY 421 GAAAAAATATTAAGAATTTTTCAGAGAGTTTGTGATACATATTTGTCCAAATGTTTCAATCA 480
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DB 421 GAAAAAATATTAAGAATTTTTCAGAGAGTTTGTGATACATATTTGTCCAAATGTTTCAATCA 480
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QY 481 ACTTCTTGA 489
    |||||||
DB 481 ACTTCTTGA 489
    |||||||

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RESULT 13
US-09-189-193-1
; Sequence 1, Application US/09189193
; Patent No. 6184359
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Anderson, Dirk
; APPLICANT: Eisenman, June

```

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RESULT 12
US-09-196-427-2
; Sequence 2, Application US/09196427
; Patent No. 6177079
; GENERAL INFORMATION:
; APPLICANT: Grabstein, Kenneth
; APPLICANT: Paxton, Raymond
; APPLICANT: Pettit, Dean
; TITLE OF INVENTION: Antagonists of IL-15
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: Word for Windows 95, 7.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,427

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APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: Seed and Berry
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/189,193
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McWaters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
US-09-189-193-1

Query Match 100.0%; Score 489; DB 4; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60
DB 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCTAAACAGAACCACTGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 GCAGGGCTTCCTAAACAGAACCACTGGTGAATGTAATAGTATTTGAAAAAATTT 180
QY 181 GAAGATCTTATTCATCAATGATATTTGATGCTACTTTATATACGGAAGTGTGTTTAC 240
DB 181 GAAGATCTTATTCATCAATGATATTTGATGCTACTTTATATACGGAAGTGTGTTTAC 240
QY 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTTCACTT 300
DB 241 CCCAGTTGCAAGTACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTATTTTCACTT 300
QY 301 GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAACTGTATCTCTAGCAACAAC 360
DB 301 GAGTCCGGAGATCAAGTATTCATGATACAGTAGAAAACTGTATCTCTAGCAACAAC 360
QY 361 AGTTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATCTGAGGAAC 420
DB 361 AGTTTCTCTTCTTAATGGGAATGTAACAGAAATCTGGATGCAAGAAATCTGAGGAAC 420

QY 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
DB 421 GAAAAAATATTAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTTCATCAAC 480
QY 481 ACTTCTTTGA 489
DB 481 ACTTCTTTGA 489
RESULT 14
PCT-US94-03793-4
Sequence 4. Application PC/TUS9403793
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Interleukin-15
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/03793
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lauener, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 489 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..489
PCT-US94-03793-4

Query Match 100.0%; Score 489; DB 5; Length 489;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60
DB 1 ATGAGAAATTCGAAACACATTTGAGAAGTATTTCCATCCAGTGCCTACTGTGTTTACTT 60
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
DB 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
QY 121 GCAGGGCTTCCTAAACAGAACCACTGGTGAATGTAATAGTATTTGAAAAAATTT 180
DB 121 GCAGGGCTTCCTAAACAGAACCACTGGTGAATGTAATAGTATTTGAAAAAATTT 180
QY 181 GAGATCTTATTCATCAATGATATTTGATGCTACTTTATATACGGAAGTGTGTTTCAC 240

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: September 19, 2002, 20:23:50 ; Search time 1617.81 Seconds
(without alignments)
4079.596 Million cell updates/sec

Title: US-09-196-427-2
Perfect score: 489
Sequence: 1 ATGAGATTTCGAACACCA.....TGTTTCATCAACACWTCCTTGA 489

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estinu:*
5: em_estov:*
6: em_estopl:*
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12: gb_gss:*
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14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	430.2	88.0	994	9	AL572832
3	399.4	81.7	509	9	AA463370
4	348.8	71.3	800	10	BG184658
5	295.8	60.5	637	9	AI860008
6	292	59.7	756	10	BI832895
7	244	49.9	872	10	BI758686
8	210.6	43.1	826	10	BI685688
9	176.2	36.0	309	10	BF095213
10	174	35.6	471	10	N76741
11	166.6	34.1	690	9	AI596704
12	152.8	31.2	474	10	N49734
13	150.2	30.7	538	9	AI152482
14	150	30.7	515	10	BF704348
15	148.2	30.3	564	9	AA863763
16	139.6	28.5	631	9	BB661271
17	132.4	27.1	166	10	BF379349

18	116	23.7	181	9	AA497102
19	107.2	21.9	817	10	BI756810
20	106.2	21.7	590	9	AA544986
21	105.8	21.6	458	9	BB825167
22	103.2	21.1	430	9	AA858938
23	98.2	20.1	420	10	BE690327
24	90	18.4	550	10	BE698667
25	87.6	17.9	429	9	AA863979
26	86.2	17.6	648	9	AA874636
27	86	17.6	718	10	BI766231
28	83	17.0	434	9	AI503618
29	82	16.8	494	9	AW804168
30	75.6	15.5	405	9	AW121388
31	75.4	15.4	301	10	BF088290
32	74.4	15.2	509	9	AI120615
33	73.8	15.1	275	10	BF088272
34	72	14.7	483	9	AW804165
35	56	11.5	391	12	AZ334843
36	55.8	11.4	278	9	BE177883
37	49.8	10.2	987	12	CNS014PQ
38	44	9.0	1101	12	CNS0039G
39	43.2	8.8	740	10	BM167297
40	43	8.7	1310	12	CNS015ZW
41	42.4	8.7	1204	12	CNS016E2
42	42.2	8.6	1101	12	CNS008WZ
43	42	8.6	1101	12	CNS017KX
44	41.2	8.4	1010	12	CNS07BNJ
45	41	8.4	998	12	CNS00LOZ

ALIGNMENTS

RESULT 1

AL548180
LOCUS
DEFINITION
AL548180 LRI_NFL006_PL2 982 bp mRNA linear EST 16-FEB-2001
prime, mRNA sequence.
ACCESSION
AL548180
VERSION
AL548180.1 GI:12882943
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 982)
AUTHORS
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE
Full-length cDNA libraries and normalization
JOURNAL
Unpublished (2001)
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES
Location/Qualifiers
1..982
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODI034Y009"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 275 a 208 c 214 g 284 t

ORIGIN

Query Match 100.0%; Score 489; DB 9; Length 982;
 Best Local Similarity 100.0%; Pred. No. 1.8e-104;
 Matches 489; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGAAATTCGAAACACATTTGAGAACTATTTCATCCAGTGCATGCTGTTTACTT 60
 Db 358 ATGAGAAATTCGAAACACATTTGAGAACTATTTCATCCAGTGCATGCTGTTTACTT 417

QY 61 CTAAACAGTCATTTCTAACTGAAGCTGCATTCATGCTTCTCATTTTGGGCTGTTTCACT 120
 Db 418 CTAAACAGTCATTTCTAACTGAAGCTGCATTCATGCTTCTCATTTTGGGCTGTTTCACT 477

QY 121 CGAGGCTTCCTAAACAGAACGCAACTGGTGAATGTAATAGTGAATTTGAAAAAAT 180
 Db 478 CGAGGCTTCCTAAACAGAACGCAACTGGTGAATGTAATAGTGAATTTGAAAAAAT 537

QY 181 GAAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTTCAC 240
 Db 538 GAAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTTCAC 597

QY 241 CCCAGTGCAGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTTATTTCACTT 300
 Db 598 CCCAGTGCAGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTTATTTCACTT 657

QY 301 GAGTCGGAGATGCAAGTATTCATGATACAGTACAGTAAAGTCTGATCATCTAGCAACAC 360
 Db 658 GAGTCGGAGATGCAAGTATTCATGATACAGTACAGTAAAGTCTGATCATCTAGCAACAC 717

QY 361 AGTTGTCTCTTAATGGGAATGTAACAGAACTGCGATGCAAGAAATGTCAGGAAGTGGAG 420
 Db 718 AGTTGTCTCTTAATGGGAATGTAACAGAACTGCGATGCAAGAAATGTCAGGAAGTGGAG 777

QY 421 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 480
 Db 778 GAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTCATCAAC 837

QY 481 ACTTCTTGA 489
 Db 838 ACTTCTTGA 846

RESULT 2
 LOCUS AL572832/C
 DEFINITION AL572832 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI034Y009 3 prime, mRNA sequence.
 ACCESSION AL572832
 VERSION AL572832.1 GI:12931481
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 994)
 AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 FEATURES
 source Location/Qualifiers
 1. .994
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DI034Y009"
 /clone_lib="LTI_NFL006_PL2"
 /tissue_type="placenta"
 /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6

vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 333 a 186 c 154 g 316 t 5 others
 ORIGIN

Query Match 88.0%; Score 430.2; DB 9; Length 994;
 Best Local Similarity 98.6%; Pred. No. 1e-90;
 Matches 429; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 55 TTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCAATCATGCTCTTCAATTTGGGCTGT 114
 Db 994 TTACTTCTAAACAGTCATTTCTAACTGAAGCTGGCAATCATGCTCTTCAATTTGGGCTGT 935

QY 115 TTCACTGCGAGGCTTCCTAAACAGAACGCAACTGGTGAATGTAATAGTGAATTTGAAA 174
 Db 934 TTCACTGCGAGGCTTCCTAAACAGAACGCAACTGGTGAATGTAATAGTGAATTTGAAA 875

QY 175 AAAATTGAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTAT 234
 Db 874 AAAATTGAGATCTTATCAATCTATGATATGATGCTACTTTATATACGGAAGTGTAT 815

QY 235 GTTACCCCGAGTGCAGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTATT 294
 Db 814 GTTACCCCGAGTGCAGAAAGTAAACAGCAATGAAGTCTTCTCTTGGAGTTACAAAGTATT 755

QY 295 TCACCTGAGTCCGGAGATGCAAGTATTCATGATACAGTAAAGTCTGATCATCTCAGCA 354
 Db 754 TCACCTGAGTCCGGAGATGCAAGTATTCATGATACAGTAAAGTCTGATCATCTCAGCA 695

QY 355 AACACAGTGTCTCTTCTAAATGGGAATGTAACAGAACTGCGATGCAAGAAATGTCAGGAA 414
 Db 694 AACACAGTGTCTCTTCTAAATGGGAATGTAACAGAACTGCGATGCAAGAAATGTCAGGAA 635

QY 415 CTGGAGGAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTC 474
 Db 634 CTGGAGGAAAAAATATTAAAGAAATTTTTCAGAGTTTGTACATATTGTCCAAATGTTTC 575

QY 475 ATCAACACTTCTTGA 489
 Db 574 ATCAACACTTCTTGA 560

RESULT 3
 LOCUS AA463370
 DEFINITION AA463370 zx97d12.r1 Soares_NHMPu.S1 Homo sapiens cDNA clone IMAGE:811703 5' similar to SW:IL15_HUMAN P40933 INTERLEUKIN-15 PRECURSOR ;, mRNA sequence.
 ACCESSION AA463370
 VERSION AA463370.1 GI:2188254
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 509)
 AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
 TITLE WashU-Merck EST Project 1997
 JOURNAL Unpublished (1997)
 COMMENT Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL : contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: similarity on wrong strand Seq primer: -28m3 rev2 ET from Amersham High quality sequence stop: 416.

FEATURES

Source
1. 509
/organism="Homo sapiens"
/db_xref="GDB:6042614"
/db_xref="taxon:9606"
/clone="IMAGE:811703"
/clone_lib="Soares_NhMPu_S1"
/tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NBM, pregnant uterus NHPU, and fetal heart NHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479."
149 a 91 c 108 g 161 t

BASE COUNT

ORIGIN

Query Match 81.7%; Score 399.4; DB 9; Length 509;
Best Local Similarity 99.8%; Pred. No. 1.6e-83;
Matches 400; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGATTTTCGAAACACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60
DB 105 ATGAGATTTTCGAAACACATTTGAGAGTATTTCCATCCAGTGTACTTGTGTTACTT 164
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTCTTCAATTTTGGGCTGTTTCAGT 120
DB 165 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTCTTCAATTTTGGGCTGTTTCAGT 224
QY 121 GCAGGGCTTCTAAACAGAGCAACTGGTGAATGTAATAGTATTAATAGTATTTGAAAAAATT 180
DB 225 GCAGGGCTTCTAAACAGAGCAACTGGTGAATGTAATAGTATTAATAGTATTTGAAAAAATT 284
QY 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTATTCAC 240
DB 285 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTATTCAC 344
QY 241 CCCAGTGGCAAGTACAGCAATGAAGTGTCTTCTCTGGAGTTACAAGTTATTTCACTT 300
DB 345 CCCAGTGGCAAGTACAGCAATGAAGTGTCTTCTCTGGAGTTACAAGTTATTTCACTT 404
QY 301 GAGTCGGAGATCAAGTATTCATGATACAGTAAAGTCTGATCATCTCCTAGCAACAAC 360
DB 405 GAGTCGGAGATCAAGTATTCATGATACAGTAAAGTCTGATCATCTCCTAGCAACAAC 464
QY 361 AGTTTCGCTTCTAATGGGATGTAAACAGATCTGGATGCAA 401
DB 465 AGTTTCGCTTCTAATGGGATGTAAACAGATCTGGATGCAA 505

RESULT

BG184658

LOCUS

DEFINITION

RST3720 Athersys RAGE Library Homo sapiens linear EST 21-APR-2001

ACCESSION

BG184658

VERSION

BG184658.1 GI:13706473

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

FEATURES

source

1. .800

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="Athersys RAGE Library"

/cell_line="HT1080"

/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

BASE COUNT 235 a 151 c 165 g 247 t 2 others

ORIGIN

Query Match 71.3%; Score 348.8; DB 10; Length 800;
Best Local Similarity 90.4%; Pred. No. 1.2e-71;
Matches 441; Conservative 0; Mismatches 37; Indels 10; Gaps 6;

QY 1 ATGAGATTTTCGAAACACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 60
DB 265 ATGAGATTTTCGAAACACATTTGAGAAGTATTTCCATCCAGTGTACTTGTGTTACTT 324
QY 61 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTCTTCAATTTTGGGCTGTTTCAGT 120
DB 325 CTAACAGTCATTTTCTAACTGAAGTGGCATTGCTCTTCAATTTTGGGCTGTTTCAGT 384
QY 121 GCAGGGCTTCTAAACAGAGCAACTGGTGAATGTAATAGTATTAATAGTATTTGAAAAAATT 180
DB 385 GCAGGGCTTCTAAACAGAGCAACTGGTGAATGTAATAGTATTTGAAAAAATT 444
QY 181 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTATTCAC 240
DB 445 GAAGATCTTATTCATCTATGCTATTTGATGCTACTTTATATACGGAAGTGTATTCAC 504
QY 241 CCCAGTGGCAAGTACAGCAATGAAGTGTCTTCTCTGGAGTTACAAGTTATTTCACTT 300
DB 505 CCCAGTGGCAAGTACAGCAATGAAGTGTCTTCTCTGGAGTTACAAGTTATTTCACTT 564
QY 301 GAGTCGGAGATCAAGTATTCATGATACAGTAAAGTCTGATCATCTCCTAGCAACAAC 360
DB 565 GAGTCGGAGATCAAGTATTCATGATACAGTAAAGTCTGATCATCTCCTAGCAACAAC 622
QY 361 AGTTTCGCTTCTAATGGGATGTAAACAGATCTGGATGCAAAGAAATGTGAGGAACCTGGAG 420
DB 623 A-TTTGGCTTCTAATGGGATGGT---ACAAAATCTGCTGCAAGAATGGAAGGACCTGAAG 678
QY 421 GAAAAAATATTAAGAAATTTTCCACAGTTTGTACATATTTGTCCTCAAAATGTTCTCAAC 480
DB 679 G--AAAAATTTTAAAGAAATTTTGAAGAAGTTTGGCCCTATTGG--CCAATGGTTCTCAAC 734
QY 481 ACTTCTTG 488
DB 735 ACTTTTGG 742

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

1 (bases 1 to 800)

Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J., and Ducar, M.

Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
21227151

Contact: Scott J. Cain

Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scain@athersys.com

High quality sequence stop: 444.


```

QY 474 CATCAACACTTCTTGA 489
Db 299 CATCAACACTTCTTGA 314

RESULT 7
BI758686
LOCUS 872 bp mRNA linear EST 25-SEP-2001
DEFINITION 603424240F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5194977 5',
mRNA sequence.
ACCESSION BI758686
VERSION BI758686
KEYWORDS EST, human.
SOURCE Homo sapiens
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 872)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11487 row: 0 column: 10
High quality sequence start: 24
High quality sequence stop: 859.
High quality sequence stop: 859.
Location/Qualifiers
1. .872
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5194977"
/clone_lib="NIH_MGC_114"
/lab_host="DH10B"
/notes="Organ: Brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."
BASE COUNT 200 a 222 c 227 g 223 t
ORIGIN

Query Match 49.9%; Score 244; DB 10; Length 872;
Best Local Similarity 98.9%; Pred. No. 4.1e-47;
Matches 277; Conservative 0; Mismatches 0; Indels 3; Gaps 3;

QY 1 ATGAGAAATTCGAACACATTTGAGAAGTATTCATCCAGTCGCTACTTGTGTACTT 60
Db 592 ATGAGAAATTCGAACACACATTTGAGAAGTATTTCCATCCAGTCGCTACTTGTGTACTT 651
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 120
Db 652 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 711
QY 121 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGTAATAGTGATTTGA-AAAAAAT 179
Db 712 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGTAATAGTGATTTGACAAAAAT 771
QY 180 TGAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTGAATGTTCA 239
Db 772 TGAAGATCTTATCAATCTATGATATTTATGCTACTTTATATACGGAAGTGAATGTTCA 831

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QY 240 -CCCCAGTTCCAAAGTAACA-GCAATGCAAGTCTTCTCT 277
Db 832 CCCCCAGTTCCAAAGTAACAAGCAATGAGTCTTCTCT 871

RESULT 8
BI685688
LOCUS 826 bp mRNA linear EST 18-SEP-2001
DEFINITION 603309529F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5345382 5',
mRNA sequence.
ACCESSION BI685688
VERSION BI685688
KEYWORDS EST, house mouse.
SOURCE Mus musculus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11877 row: j column: 07
High quality sequence stop: 826.
High quality sequence stop: 826.
Location/Qualifiers
1. .826
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:5345382"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 212 a 218 c 174 g 222 t
ORIGIN

Query Match 43.1%; Score 210.6; DB 10; Length 826;
Best Local Similarity 79.4%; Pred. No. 2.7e-39;
Matches 274; Conservative 0; Mismatches 69; Indels 2; Gaps 2;

QY 1 ATGAGAAATTCGAACACATTTGAGAAGTATTTCCATCCAGTCGCTACTTGTGTACTT 60
Db 481 ATGAGAAATTCGAACACATATATAGGAATACATCCATCTCGTCTACTTGTGTACTT 540
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 120
Db 541 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATGCTTCATTTGGGCTGTTTCAGT 599
QY 121 GCAGGGCTTCTTAAACAGAACCACTGGGTGAATGTAATAGTGATTTGAAAAAAT 180
Db 600 GTAGGTCTCCCTAAACAGAGGCCAAGTGGATAGATATGACCTGGAGAAAAAT 659
QY 181 GAAGATCTTATCAATCTATCCATATTTGATGCTCTATTATATACGGAAGTGTTCAC 240
Db 660 GAAAGCTTATCAATCTATTTTCATA-TGACACCACTTATATACAGTGAAGTGTTCAT 718
QY 241 CCCAGTTGCAAGTAACAGCAATGAAGTGTCTTCTTGGAGTTTACAAGTGTATTTCACTT 300

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Db 121 TATTAAGAATTTTGCAGAGTTTGTACATATTGCCAAATGTTTCATCAACACTTCTTG 180
QY 489 A 489
Db 181 A 181

RESULT 10
N76741
LOCUS N76741 471 bp mRNA linear EST 02-APR-1996
DEFINITION yz82g12.r1 Soares_multiple_sclerosis_2NbHSP Homo sapiens cDNA
clone IMAGE:289606 5' similar to SW:IL15_HUMAN P40933
INTERLEUKIN-15 PRECURSOR ; mRNA sequence.
ACCESSION N76741
VERSION N76741.1 GI:12393919
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 471)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
,R., Williamson,A., Wohldmann,P. and Willson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: reverse ET
High quality sequence stop: 296.
Location/Qualifiers
1..471
/organism="Homo sapiens"
/db_xref="GDB:3905446"
/db_xref="taxon:9606"
/clone="IMAGE:289606"
/clone_lib="Soares_multiple_sclerosis_2NbHSP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT7p3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site.1: Not I; Site.2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer 15'
TTTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTT 3'
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT7p3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."
BASE COUNT 161 a 68 c 83 g 154 t 5 others
ORIGIN

Query Match 35.6%; Score 174; DB 10; Length 471;
Best Local Similarity 97.4%; Pred. No. 9.8e-31;
Matches 185; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 301 GATCCGGAGATCGAAGTATTCATGATACAGTAGAATAATCTGATCATCTAGCAACAC 360
Db 4 GAGTCGGAGATCGAAGTATTCATGATACAGTAGAATAATCTGATCATCTAGCAACAC 63

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QY 361 AGTTTGCTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATGTGAGGAACACTGGAG 420
|||||
Db 64 AGTTTGCTCTTAATGGGAATGTAACAGAATCTGGATGCAAGAATGTGAGGAACACTGGAG 123
|||||
QY 421 GAAAAAATATTAAAGAATTTTTCAGAGTTTGTACATATTGTCACAAATGTTTCAT-CAA 479
|||||
Db 124 GAAAAAATATTAAAGAATTTTTCAGAGTTTGTACATATTGTCACAAATGTTTCAT-CAA 183
|||||
QY 480 CACTTCTTGA 489
|||||
Db 184 CACTTCTTGA 193
|||||

RESULT 11
LOCUS AI596704
DEFINITION VK38b11.v1 Soares_mammary_gland_NbMMG Mus musculus cDNA clone
IMAGE:948933 5' similar to gb:U14332 Mus musculus Interleukin 15
(MOUSE), mRNA sequence.
ACCESSION AI596704
VERSION AI596704
KEYWORDS EST
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 690)
NCI-CCAP http://www.ncbi.nlm.nih.gov/nciccap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:545789
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 466.
FEATURES
Location/Qualifiers
1..690
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:948933"
/clone_lib="Soares_mammary_gland_NbMMG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/notes="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia
) with a modified polylinker; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dr)
primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGCAATGGTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."
178 a 177 c 158 g 170 t 7 others

BASE COUNT
ORIGIN

Query Match 34.1%; Score 166.6; DB 9; Length 690;
Best Local Similarity 81.5%; Pred. No. 5.4e-29;
Matches 190; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1 ATGAGATTTTGAACACATTTGAGAGATATTTCACATCCAGTCTACTGTGTTTACTT 60

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Db 450 ATGAAAATTTGAAACCATATATAGGAATACATCCATCTCGTCTACTTGTGTTCTT 509
|||||
QY 61 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 120
|||||
Db 510 CTAACAGTCATTTTCTAACTGAAGCTGGCATTCATCTCTTCAATTTGGGCTGTTTCAGT 569
|||||
QY 121 CGAGGGCTTCTTAAACAGAGCCAACTGGGTGAATGTAATAAGTATTTGAAAAAAATT 180
|||||
Db 570 GTAGGTCTCCCTAAACAGAGCCAACTGGGTGAATGTAATAAGTATTTGAAAAAAATT 629
|||||
QY 181 GAGATCTTATTCATCTATGATTCATCTACTTATATACGGAAGTGA 233
|||||
Db 630 GAAAGCCTTATTCATCTATGATTCATCTACTTATATACGGAAGTGA 682
|||||

RESULT 12
LOCUS N49734/c
DEFINITION Y206b12.s1 Soares_multiple_sclerosis_2NbHMP Homo sapiens cDNA
clone IMAGE:282239 3' similar to SW:IL15_HUMAN P40933
INTERLEUKIN-15 PRECURSOR ; , mRNA sequence.
ACCESSION N49734
VERSION N49734.1 GI:1190900
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
REFERENCE Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman
, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J.,
Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston
, R., Williamson, A., Wohldmann, P. and Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 263.
FEATURES
Location/Qualifiers
1..474
/organism="Homo sapiens"
/db_xref="GDB:3900767"
/db_xref="taxon:9606"
/clone="IMAGE:282239"
/clone_lib="Soares_multiple_sclerosis_2NbHMP"
/sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/notes="Vector: pT73D (Pharmacia) with a modified
polylinker V.TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dr)
primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGCAATGGTTTTTTTTTTTTTTTT
T 3']; double-stranded cDNA was size selected, ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH)."
160 a 81 c 67 g 161 t 5 others

BASE COUNT
ORIGIN

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Query Match 31.2%; Score 152.8; DB 10; Length 474; Mismatches 0; Gaps 0;
 Best Local Similarity 95.7%; Pred. No. 9e-26;
 Matches 154; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 329 CAGTAAAGATGATCATCTAGCAACAAACAGTTTCTCTTAATGGGAATGTAACAG 388
 DB 473 CAGTAGGAATGATCATCTAGCAACAAACAGTTTCTCTTAATGGGAATGTAACAG 414
 QY 389 AATCTGATGCAAGAAATGTGAGGAATGTGAGGAAGAAATATTAAGAAATTTTGCAGA 448
 DB 413 AATCTGATGCAAGAAATGTGAGGAATGTGAGGAAGAAATATTAAGAAATTTTGCAGA 354
 QY 449 GTTTTGTACATATGTCCAAATGTTTCATCAACACTTCTTGA 489
 DB 353 GTTTTGTACATATGTCCAAATGTTTCATCAACACTTCTTGA 313

RESULT 13 AII52482/c

LOCUS AII52482 538 bp mRNA linear EST 30-SEP-1998
 DEFINITION ud83d09.r1 Soares_mammary_gland_NMLMG Mus musculus cDNA clone
 IMAGE:1477457 5' similar to gb:U14332 Mus musculus interleukin 15
 (MOUSE);, mRNA sequence.

ACCESSION AII52482.1 GI:3680951

VERSION EST.

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 538)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:925813

Seq primer: -28ml3 rev2 ET from Amersham

High quality sequence stop: 326.

Location/Qualifiers

1. 538

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="IMAGE:1477457"

/clone_lib="Soares_mammary_gland_NMLMG"

/sex="female (lactating)"

/tissue_type="mammary gland"

/lab_host="DH10B"

/note="vector: pMT3D-Pac (Pharmacia) with a modified

polylinker; 1st strand cDNA was prepared from mammary

gland tissue from a lactating female, and was then primed

with a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not

I and cloned into the Not I and Eco RI sites of the

modified pMT3 vector. Library is normalized. Library

was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 163 a 108 c 103 g 163 t 1 others

ORIGIN

Best Local Similarity 76.1%; Pred. No. 3.7e-25;
 Matches 185; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 247 TCGAAGTAACAGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCC 306
 DB 532 TCGAAGTACTGCAATGAAGTCTTCTCTTGGAGTTACAAGTTATTTCACCTTGAGTCC 473
 QY 307 GCGAGATGCAAGTATTCATGATACAGTAGAAGTCTGATCATCTAGCAACAAACAGTTTG 366
 DB 472 ACTACATGACTCTTANTGAACAGTAGAAGTCTGATCATCTAGCAACAAACAGTCTG 413
 QY 367 TCTTCTAATGGAATGTACAGAAATCTGGATCAAGAAATGTGAGAACTGGAGGAAAA 426
 DB 412 TCTTCTAAGAAATGTACAGAAATCTGGATCAAGAAATGTGAGGAGTGGAGGAGAA 353
 QY 427 AATATTAAAGAAATTTTGCAGAGTTTGTACATATTTGCCAAATGTTCATCAACACTTCT 486
 DB 352 ACCTTACAGAGTTTTTGCAGAGTTTGTACATATTTGCCAAATGTTCATCAACACTTCT 293
 QY 487 TGA 489
 DB 292 TGA 290

RESULT 14 BF704348/c

LOCUS BF704348

DEFINITION MI-P-03-aba-f-02-1-UM.s1 MI-P-03 Sus scrofa cDNA clone

ACCESSION BF704348

VERSION BF704348.1 GI:11989750

KEYWORDS EST.

SOURCE pig.

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 515)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

Contact: Tuggle CK

Molecular Genetics Laboratory, Department of Animal Science

Iowa State University

201 Kildes Hall, Ames, IA 50011-3150, USA

Tel: 5152944252

Fax: 5152942401

Email: cktuggle@iastate.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to verify it as a clone from the

non-normalized ovary at estrus day 12 library cDNA library

Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science

Research Center, Department of Animal Science, University of

Missouri-Columbia, 65211 clone distribution: clones will be

available through Research Genetics (www.resgen.com) The following

repetitive elements were found in this cDNA sequence: 1-28,

>AT-richlow.complexity 81-112, >AT-richlow.complexity

Seq primer: M13 Forward

POLYA=Yes.

Location/Qualifiers

1. 515

/organism="Sus scrofa"

/strain="crossbreed"

/db_xref="taxon:9823"

/clone="MI-P-03-aba-f-02-1-UM"

/clone_lib="MI-P-03"

/lab_host="DH10B (Life Technologies)"

/note="vector: pMT3D-Pac (Pharmacia) with a modified

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

polylinker; Site_1: Not I; Site_2: EcoRI; the MI-P-03

Search completed: September 19, 2002, 22:49:12
Job time: 8722 sec

